

GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: April 14, 2003, 09:31:34 ; Search time 523.667 Seconds  
(without alignments)  
1500.527 Million cell updates/sec

Title: US-09-821-734-12

Perfect score: 27

Sequence: 1 ctccttcacgaaacgactcggtgtg 27

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

GenEmbl:\*

- 1: gb\_ba:\*
- 2: gb\_htg:\*
- 3: gb\_in:\*
- 4: gb\_on:\*
- 5: gb\_ov:\*
- 6: gb\_pat:\*
- 7: gb\_ph:\*
- 8: gb\_pl:\*
- 9: gb\_pt:\*
- 10: gb\_ro:\*
- 11: gb\_sts:\*
- 12: gb\_sy:\*
- 13: gb\_un:\*
- 14: gb\_vl:\*
- 15: em\_ba:\*
- 16: em\_fun:\*
- 17: em\_hum:\*
- 18: em\_in:\*
- 19: em\_mu:\*
- 20: em\_on:\*
- 21: em\_or:\*
- 22: em\_ov:\*
- 23: em\_pat:\*
- 24: em\_ph:\*
- 25: em\_pl:\*
- 26: em\_ro:\*
- 27: em\_sts:\*
- 28: em\_un:\*
- 29: em\_vl:\*
- 30: em\_htg\_hum:\*
- 31: em\_htg\_inv:\*
- 32: em\_htg\_other:\*
- 33: em\_htg\_mus:\*
- 34: em\_htg\_pln:\*
- 35: em\_htg\_rtd:\*
- 36: em\_htg\_mam:\*
- 37: em\_htg\_wrt:\*
- 38: em\_sy:\*
- 39: em\_htgo\_hum:\*
- 40: em\_htgo\_mus:\*
- 41: em\_htgo\_other:\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	27	100.0	27	6	AX268374	AX268374 Sequence
2	27	100.0	127	11	AF008934	AF008934 Homo sapi
3	27	100.0	129	9	HSU93599	U93599 Homo sapien
4	27	100.0	444	11	G53000	G53000 SHGC-81785
5	27	100.0	1641	9	AF107214	AF107214 Homo sapi
6	27	100.0	2253	6	AX467227	AX467227 Sequence
7	27	100.0	2253	9	AY101595	AY101595 Homo sapi
8	27	100.0	2472	9	BC025672	BC025672 Homo sapi
9	27	100.0	2518	9	AF176574	AF176574 Homo sapi
10	27	100.0	2558	6	AX376036	AX376036 Sequence
11	27	100.0	2653	6	AX337498	AX337498 Sequence
12	27	100.0	2653	6	123794	123794 Sequence 1
13	27	100.0	2653	9	HUMPSM	M99487 Human prost
14	27	100.0	93525	9	AF007544	AF007544 Homo sapi
15	27	100.0	117521	2	AC023784	AC023784 Homo sapi
16	27	100.0	129095	9	AC110742	AC110742 Homo sapi
17	27	100.0	158524	2	AL162372	AL162372 Homo sapi
18	27	100.0	187638	2	AC118273	AC118273 Homo sapi
19	23	85.2	198	9	AF016826	AF016826 Homo sapi
20	20.6	76.3	199052	2	AC122962	AC122962 Rattus no
21	20.2	74.8	246865	2	AC074003	AC074003 Homo sapi
22	19.8	73.3	2532	4	AF050502	AF050502 Sus scrof
23	19.2	71.1	119451	2	AP003958	AP003958 Oryza sat
24	19.2	71.1	125687	2	AP004743	AP004743 Oryza sat
25	19.2	71.1	332635	1	AP003005	AP003005 Mesorhizo
26	19	70.4	51920	2	CER08A5	282281 Caenorhabdi
27	19	70.4	130027	9	AC004982	AC004982 Homo sapi
28	19	70.4	133402	9	AL137843	AL137843 Human DNA
29	18.6	68.9	64920	1	AE008925	AE008925 Xanthomon
30	18.6	68.9	93294	9	AL607144	AL607144 Human DNA
31	18.6	68.9	142762	2	AL391599	AL391599 Homo sapi
32	18.6	68.9	161456	2	AC078869	AC078869 Homo sapi
33	18.6	68.9	171968	2	AC125965	AC125965 Rattus no
34	18.6	68.9	184480	2	AC016887	AC016887 Homo sapi
35	18.6	68.9	214793	2	AC023345	AC023345 Homo sapi
36	18.6	68.9	216599	2	AC087379	AC087379 Homo sapi
37	18.6	68.9	306050	1	RME603645	AL603645 Rhizobium
38	18.4	68.1	1071	5	AF168111	AF168111 Piaya mel
39	18.4	68.1	349980	6	AX344571	AX344571 Sequence
40	18.4	68.1	349980	6	AX344572	AX344572 Sequence
41	18.2	67.4	9704	2	AC017694	AC017694 Drosophil
42	18.2	67.4	19750	3	AE002980	AE002980 Drosophil
43	18.2	67.4	204167	2	AC110553	AC110553 Mus muscu
44	18	66.7	208	9	HSLN2C55	U66787 Human lamin
45	18	66.7	424	9	HSA323185	AJ323185 Homo sapi

ALIGNMENTS

RESULT 1	AX268374	AX268374	Sequence 12 from Patent WO0174845.	27 bp	DNA	linear	PAT 29-OCT-2001
LOCUS	AX268374	AX268374	Sequence 12 from Patent WO0174845.				
DEFINITION	AX268374	AX268374	Sequence 12 from Patent WO0174845.				
ACCESSION	AX268374	AX268374	Sequence 12 from Patent WO0174845.				
VERSION	AX268374.1	GI:16541581					
KEYWORDS							
SOURCE			synthetic construct.				
ORGANISM			synthetic construct				
REFERENCE			artificial sequences.				
AUTHORS			1				
TITLE			Pedyczak A., Chong P. and Sia C.D.				
JOURNAL			Immunogenic peptides derived from prostate-specific membrane antigen (psma) and uses thereof				
			Patent: WO 0174845-A 12 11-OCT-2001;				

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FEATURES
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        /note="CLP326"
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Db 1 CTCCTTCACGAACCGACTCGGCTGTG 27

RESULT 2
AF008934
LOCUS      AF008934      127 bp      DNA      linear      STS 16-SEP-1997
DEFINITION Homo sapiens prostate-specific membrane antigen related sequence,
            sequence tagged site.
ACCESSION  AF008934
VERSION     AF008934.1 GI:2393914
KEYWORDS   STS.
SOURCE     Homo sapiens.
  ORGANISM
    Homo sapiens
      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
    1 (bases 1 to 127)
  AUTHORS   Maraj,B.H., Whelan,P. and Markham,A.F.
  TITLE     Prostate-Specific Membrane Antigen Related Gene
  JOURNAL   Unpublished
  REFERENCE 2 (bases 1 to 127)
  AUTHORS   Maraj,B.H., Whelan,P. and Markham,A.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-JUN-1997) Molecular Medicine Unit, Leeds University,
            Beckett, Leeds, Yorkshire LS9 7TF, England
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        /map="11q14"
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        /note="similar to prostate-specific membrane antigen gene"
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    Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCCTTCACGAACCGACTCGGCTGTG 27
    |||||||
Db 10 CTCCTTCACGAACCGACTCGGCTGTG 36

RESULT 3
HSU93599
LOCUS      HSU93599      129 bp      DNA      linear      PRI 05-JUL-2001
DEFINITION Homo sapiens PSM pseudogene, partial sequence.
ACCESSION  U93599
VERSION     U93599.1 GI:1928993
KEYWORDS
SOURCE     Homo sapiens.
  ORGANISM
    Homo sapiens
      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
    1 (bases 1 to 129)
  REFERENCE

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AUTHORS   Maraj,B.H., Leek,J.P., Karayi,M., Ali,M., Lench,N.J. and
            Markham,A.F.
  TITLE     Detailed genetic mapping around a putative prostate-specific
            membrane antigen locus on human chromosome 11p11.2
  JOURNAL   Cytogenet. Cell Genet. 81 (1), 3-9 (1998)
  MEDLINE   98358137
  PUBMED    9691167
  REFERENCE 2 (bases 1 to 129)
  AUTHORS   Maraj,B.H., Bailey,A., Carr,I.M. and Markham,A.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-MAR-1997) Molecular Medicine Unit, Leeds University,
            Beckett Street, Leeds, West Yorkshire LS9 7TF, England
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        /gene="PSM"
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    Best Local Similarity 100.0%; Pred. No. 0.29;
    Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCCTTCACGAACCGACTCGGCTGTG 27
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Db 10 CTCCTTCACGAACCGACTCGGCTGTG 36

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LOCUS      G53000      444 bp      DNA      linear      STS 30-MAR-2000
DEFINITION SHGC-81785 Human Homo sapiens STS genomic, sequence tagged site.
ACCESSION  G53000
VERSION     G53000.1 GI:5224177
KEYWORDS   STS.
SOURCE     Homo sapiens.
  ORGANISM
    Homo sapiens
      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
    1 (bases 1 to 444)
  AUTHORS   Olivier,M. and Cox,D.R.
  TITLE     Unpublished, Olivier, M., Cox, D.R. (2000)
  JOURNAL   Unpublished (2000)
  COMMENT   Contact: Michael Olivier, David R. Cox
            Stanford Human Genome Center
            Stanford University School of Medicine
            4005 Miranda Ave. 2nd Fl., Palo Alto, CA 94025, USA
            Tel: (650) 320-5800
            Fax: (650) 320-5801
            Email: olivier@shgc.stanford.edu
            Primer A: ACCGAGCGATTAGTGAGATTGAG
            Primer B: ACAGGAGCCGAGGAGGAGAA
            STS size: 230
            PCR Profile:
              Initial incubation: 95 degrees C for 10 minutes
              Denaturation: 94 degrees C for 30 seconds
              Annealing: 60 degrees C for 30 seconds
              Polymerization: 72 degrees C for 23 seconds
              PCR Cycles: 30
              Thermal Cycler: Perkin Elmer 9700
            Protocol:
              Template: 25 ng
              Primer: each 1 uM
              dNTPs: each 200 uM
              AmpliTaq Gold Polymerase: 0.07 units/ul
              Total Vol: 5 ul

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OM nucleic - nucleic search, using sw model

Run on: April 14, 2003, 09:27:29 ; Search time 99 seconds  
(without alignments)  
614.181 Million cell updates/sec

Title: US-09-821-734-12

Perfect score: 27

Sequence: 1 ctcttcacgaacacgactcgctgtg 27

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 4: /SID52/gcgdata/geneseq/geneseqn-embl/NA1983.DAT.\*
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- 23: /SID52/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT.\*
- 24: /SID52/gcgdata/geneseq/geneseqn-embl/NA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	27	100.0	27	22 AAS15139	Human DNA encoding
2	27	100.0	101	21 AAF16465	Human prostate can
3	27	100.0	866	21 AAF15696	Human prostate can
4	27	100.0	2253	21 AAA09454	Human prostate spe
5	27	100.0	2558	21 AAC78599	Human PRO739 nucle
6	27	100.0	2558	22 AAS45976	Human DNA encoding
7	27	100.0	2653	15 AAO65520	Prostate-specific
8	27	100.0	2653	24 ABK86204	cDNA encoding huma
9	27	100.0	2653	24 ABK64556	Human benign prost

10	27	100.0	2653	24 ABL69670	Prostate cancer re
11	27	100.0	2654	17 AAT36785	Prostate-specific
12	27	100.0	2884	23 ABV22873	Human prostate exp
13	27	100.0	2884	23 ABV23013	Human prostate exp
14	27	100.0	2884	23 ABV28703	Human prostate exp
15	27	100.0	2884	23 ABV28849	Human prostate exp
16	27	100.0	3017	17 AAT36776	Prostate-specific
17	27	100.0	3017	17 AAT36786	Prostate-specific
18	23	85.2	24	22 AAD17629	Human FGP gene sp
19	18	66.7	98	22 ABA51445	Human breast cell
20	18	66.7	98	22 ABA69473	Human foetal liver
21	18	66.7	98	22 ABA36398	Probe #14864 for g
22	18	66.7	98	22 AAK17728	Human brain expres
23	18	66.7	98	22 AAK43549	Human bone marrow
24	18	66.7	98	22 AAI24335	Probe #14268 for g
25	18	66.7	98	22 AAI49605	Probe #18291 used
26	18	66.7	98	22 AAI09877	Probe #9868 used t
27	18	66.7	98	24 ABS17686	Human genome-deriv
28	18	66.7	339	20 AAV90178	EST clone DF780.
29	18	66.7	339	20 AAV89499	EST clone COL187.
30	18	66.7	470	22 ABA46343	Human breast cell
31	18	66.7	470	22 ABA56908	Human foetal liver
32	18	66.7	470	22 ABA26523	Probe #4989 for ge
33	18	66.7	470	22 AAK05005	Human brain expres
34	18	66.7	470	22 AAK30539	Human bone marrow
35	18	66.7	470	22 AAI15155	Probe #5088 for ge
36	18	66.7	470	22 AAI36483	Probe #5169 used t
37	18	66.7	470	22 AAI04898	Probe #4889 used t
38	18	66.7	470	24 ABS05182	Human genome-deriv
39	18	66.7	3554	12 AAO13225	Merosin gene. Hom
40	18	66.7	3554	16 AAO86479	Merosin partial cD
41	18	66.7	4408	24 ABL61776	Colon adenocarcino
42	18	66.7	4598	24 ABK35727	cDNA sequence #118
43	18	66.7	9419	21 AAA88894	Human laminin 2 al
44	18	66.7	9420	21 AAA88892	Human laminin 2 al
45	18	66.7	9534	16 AAT17419	Merosin cDNA. Hom

ALIGNMENTS

RESULT 1  
AAS15139  
ID AAS15139 standard; DNA; 27 BP.

XX AAS15139;

XX 16-JAN-2002 (first entry)

XX Human DNA encoding a PSMA derived immunogenic peptide CLP326.

XX Human; ds; PSMA; prostate specific membrane antigen; prostate cancer;

XX tumour; immunogenic peptide; cytostatic; gene therapy; CLP326.

XX Homo sapiens.

XX Key Location/Qualifiers

FT CDS 1..27

FT /tag= a

FT /product= "CLP326"

FT /partial

FT /note= "No start or stop codon"

XX WO200174845-A2.

XX 11-OCT-2001.

XX 30-MAR-2001; 2001WO-CA00411.

XX 31-MAR-2000; 2000US-193386P.

XX (AVET ) AVENTIS PASTEUR LTD.

PI Pedyczak A, Chong P, Sia CDY;  
 XX WPI: 2001-626378/72.  
 DR P-PSDB; AAU09104.  
 XX  
 PT New polypeptides useful for inducing an immune response and treating  
 PT prostate cancer comprises polypeptides derived from the prostate  
 PT specific membrane antigen.  
 XX  
 XX  
 PS Claim 6; Page 15; 47pp; English.  
 CC The invention relates to prostate specific membrane antigen (PSMA)  
 CC derived peptides (and the nucleic acids encoding them) capable of  
 CC eliciting an immune response. The molecules of the invention are used to  
 CC elicit an immune response, particularly to treat cancer and tumours,  
 CC especially prostate cancer. Delivery of the peptides may be by  
 CC expression from the nucleic acids encoding them (i.e. gene therapy).  
 CC The present sequence encodes a PSMA derived immunogenic peptide.  
 XX  
 XX Sequence 27 BP; 5 A; 10 C; 6 G; 6 T; 0 other;  
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 Query Match 100.0%; Score 27; DB 22; Length 27;  
 Best Local Similarity 100.0%; Pred. No. 0.0023;  
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CTCCTTCACGAAACCGACTCGGCTGTG 27  
 Db 1 CTCCTTCACGAAACCGACTCGGCTGTG 27  
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 AC AAF16465;  
 XX  
 DT 13-MAR-2001 (first entry)  
 DE Human prostate cancer antigen nucleotide sequence SEQ ID NO:900.  
 KW Human; prostate cancer; prostate cancer antigen; detection; diagnosis;  
 KW neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular;  
 KW vulnery; gastrointestinal; nephrotropic; antiinfective; gynaecological;  
 KW antibacterial; gene therapy; neural; immune; reproductive; renal;  
 KW gastrointestinal; pulmonary; cardiovascular; proliferative disorder;  
 KW wound; infectious disease; ss.  
 XX Homo sapiens.  
 OS  
 XX WO200055174-A1.  
 PN  
 XX 21-SEP-2000.  
 PD  
 PF  
 XX 08-MAR-2000; 2000WO-US05988.  
 XX  
 PR 12-MAR-1999; 99US-0124270.  
 XX  
 PF (HUMA-) HUMAN GENOME SCI INC.  
 XX (ROSE/) ROSEN C A.  
 PR  
 PI Rosen CA, Ruben SM;  
 XX WPI: 2000-587513/55.  
 DR P-PSDB; AAB57262.  
 XX  
 PT Prostate cancer associated gene sequences, referred to as prostate  
 PT cancer antigens, useful for treatment, prevention, and diagnosis of  
 PT disorders such as prostate cancer.  
 XX  
 PS Claim 1; Page 1341; 2338pp; English.  
 CC AAF15566 to AAF16505 encode the human prostate cancer associated  
 CC proteins, called prostate cancer antigens, given in AAB56363 to AAB57302.  
 CC The prostate cancer antigens can have neuroprotective, cytostatic,  
 CC cardioactive, immunomodulatory, muscular, vulnery, gastrointestinal,  
 CC nephrotropic, antiinfective, gynaecological and antibacterial activities,  
 CC and can be used in gene therapy. The prostate cancer antigen  
 CC polynucleotides may be used for detection of prostate cancer, chromosome  
 CC identification, as chromosome markers, and for numerous other diagnostic  
 CC or research purposes. The prostate cancer antigens may be used to treat  
 CC disorders such as neural, immune, muscular, reproductive,  
 CC gastrointestinal, pulmonary, cardiovascular, renal, and proliferative  
 CC disorders, wounds, and infectious diseases. AAF16506 to AAF16514 to  
 CC AAB57303 represent sequences used in the exemplification of the present  
 CC invention.  
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 Best Local Similarity 100.0%; Pred. No. 0.0027;  
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CTCCTTCACGAAACCGACTCGGCTGTG 27  
 Db 61 CTCCTTCACGAAACCGACTCGGCTGTG 87  
 RESULT 3  
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 AC AAF15696;  
 XX  
 DT 13-MAR-2001 (first entry)  
 DE Human prostate cancer antigen nucleotide sequence SEQ ID NO:131.  
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 KW neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular;  
 KW vulnery; gastrointestinal; nephrotropic; antiinfective; gynaecological;  
 KW antibacterial; gene therapy; neural; immune; reproductive; renal;  
 KW gastrointestinal; pulmonary; cardiovascular; proliferative disorder;  
 KW wound; infectious disease; ss.  
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 OS  
 XX WO200055174-A1.  
 PN  
 XX 21-SEP-2000.  
 PD  
 PF  
 XX 08-MAR-2000; 2000WO-US05988.  
 XX  
 PR 12-MAR-1999; 99US-0124270.  
 XX  
 PF (HUMA-) HUMAN GENOME SCI INC.  
 XX (ROSE/) ROSEN C A.  
 PR  
 PI Rosen CA, Ruben SM;  
 XX WPI: 2000-587513/55.  
 DR P-PSDB; AAB56493.  
 XX  
 PT Prostate cancer associated gene sequences, referred to as prostate  
 PT cancer antigens, useful for treatment, prevention, and diagnosis of  
 PT disorders such as prostate cancer.  
 XX  
 PS Claim 1; Page 697-698; 2338pp; English.  
 CC AAF15566 to AAF16505 encode the human prostate cancer associated  
 CC proteins, called prostate cancer antigens, given in AAB56363 to AAB57302.  
 CC The prostate cancer antigens can have neuroprotective, cytostatic,  
 CC cardioactive, immunomodulatory, muscular, vulnery, gastrointestinal,  
 CC nephrotropic, antiinfective, gynaecological and antibacterial activities,  
 CC and can be used in gene therapy. The prostate cancer antigen  
 CC polynucleotides may be used for detection of prostate cancer, chromosome  
 CC identification, as chromosome markers, and for numerous other diagnostic

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OM nucleic - nucleic search, using sw model

Run on: April 14, 2003, 10:10:25 ; Search time 21 seconds  
(without alignments)  
394.299 Million cell updates/sec

Title: US-09-821-734-12

Perfect score: 27

Sequence: 1 ctcttcacgaacgactcgctgtg 27

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

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Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq: \*  
3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq: \*  
4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq: \*  
5: /cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq: \*  
6: /cgn2\_6/ptodata/1/ina/backfiles1.seq: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	27	100.0	2653	1 US-08-325-553-1	Sequence 1, Appli
2	27	100.0	2653	2 US-08-394-152A-1	Sequence 1, Appli
c 3	27	100.0	2957	2 US-08-394-152A-48	Sequence 48, Appli
4	27	100.0	3017	2 US-08-394-152A-39	Sequence 39, Appli
c 5	18	66.7	3554	2 US-08-460-309-1	Sequence 1, Appli
c 6	18	66.7	3554	2 US-08-125-077-1	Sequence 1, Appli
c 7	18	66.7	3554	6 5444158-1	Patent No. 5444158
8	17.4	64.4	4657	3 US-09-254-325-1	Sequence 1, Appli
9	17.4	64.4	5643	3 US-09-079-415-5	Sequence 5, Appli
10	17.4	64.4	5643	3 US-08-750-458A-1	Sequence 1, Appli
c 11	17.2	63.7	606	4 US-08-998-416-106	Sequence 106, App
c 12	17.2	63.7	718	4 US-08-998-416-611	Sequence 611, App
c 13	17.2	63.7	1809	1 US-08-204-198A-3	Sequence 3, Appli
c 14	17.2	63.7	1809	1 US-08-204-198A-4	Sequence 4, Appli
15	17	63.0	286	3 US-08-688-988-12	Sequence 12, Appli
c 16	17	63.0	628	1 US-08-686-878A-1	Sequence 1, Appli
c 17	17	63.0	1893	1 US-08-271-667B-5	Sequence 5, Appli
c 18	17	63.0	1893	3 US-08-765-889C-18	Sequence 18, Appli
c 19	17	63.0	1893	5 PCT-US95-07855-18	Sequence 18, Appli
c 20	17	63.0	2101	3 US-08-765-889C-5	Sequence 5, Appli
c 21	17	63.0	2101	5 PCT-US95-07855-5	Sequence 5, Appli
c 22	17	63.0	2166	4 US-09-175-928-1	Sequence 1, Appli
c 23	17	63.0	2304	3 US-08-271-667B-6	Sequence 6, Appli
c 24	17	63.0	2304	3 US-08-765-889C-19	Sequence 19, Appli
c 25	17	63.0	2304	5 PCT-US95-07855-19	Sequence 19, Appli
c 26	17	63.0	2430	2 US-08-820-170A-35	Sequence 35, Appli
c 27	17	63.0	2430	3 US-09-055-699-35	Sequence 35, Appli

c 28	17	63.0	2430	4 US-09-273-565-35	Sequence 35, Appli
c 29	17	63.0	2430	4 US-09-565-538-35	Sequence 35, Appli
c 30	17	63.0	2430	4 US-09-661-468-35	Sequence 35, Appli
c 31	17	63.0	2977	2 US-08-820-170A-36	Sequence 36, Appli
c 32	17	63.0	2977	3 US-09-055-699-36	Sequence 36, Appli
c 33	17	63.0	2977	4 US-09-273-565-36	Sequence 36, Appli
c 34	17	63.0	2977	4 US-09-565-538-36	Sequence 36, Appli
c 35	17	63.0	2977	4 US-09-661-468-36	Sequence 36, Appli
c 36	16.4	60.7	1454	2 US-08-657-392-1	Sequence 1, Appli
37	16.4	60.7	1454	5 PCT-US94-02539-1	Sequence 1, Appli
38	16.4	60.7	1455	2 US-08-657-392-26	Sequence 26, Appli
39	16.4	60.7	1455	5 PCT-US94-02539-26	Sequence 26, Appli
40	16	59.3	614	4 US-09-385-982-399	Sequence 399, App
c 41	16	59.3	660	4 US-08-981-030-4	Sequence 4, Appli
c 42	16	59.3	1596	1 US-08-513-841-3	Sequence 3, Appli
c 43	16	59.3	1596	2 US-08-696-834-3	Sequence 3, Appli
c 44	16	59.3	1596	2 US-08-942-673-3	Sequence 3, Appli
c 45	16	59.3	1596	4 US-09-118-317-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1  
US-08-325-553-1  
; Sequence 1, Application US/08325553  
; Patent No. 5538866  
; GENERAL INFORMATION:  
; APPLICANT: Israeli, Ron S.  
; APPLICANT: Heston, Warren D.W.  
; APPLICANT: Fair, William R.  
; TITLE OF INVENTION: THE PROSTATE-SPECIFIC MEMBRANE ANTIGEN  
; NUMBER OF SEQUENCES: 38  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooper & Dunham  
; STREET: 30 Rockefeller Plaza  
; CITY: New York  
; STATE: New York  
; COUNTRY: United States of America  
; ZIP: 10112  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/325,553  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/07/973,337A  
; FILING DATE: 05 NOV 1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White, John P.  
; REGISTRATION NUMBER: 28,678  
; REFERENCE/DOCKET NUMBER: 1747/41426  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 977-9550  
; TELEFAX: (212) 664-0525  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2653 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; ORGANISM: Homo sapiens  
; TISSUE TYPE: Carcinoma  
; IMMEDIATE SOURCE:

CLONE: Prostate-Specific Membrane Antigen  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 262..2511  
US-08-325-553-1

Query Match 100.0%; Score 27; DB 1; Length 2653;  
Best Local Similarity 100.0%; Pred. No. 0.00048;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 271 CTCCTTCACGAAACCGACTCGGCTGTG 297

RESULT 2  
US-08-394-152A-1  
; Sequence 1, Application US/08394152A  
; Patent No. 5935818  
; GENERAL INFORMATION:  
; APPLICANT: Israeli, Ron S.  
; APPLICANT: Heston, Warren D.W.  
; APPLICANT: Fair, William R.  
; TITLE OF INVENTION: PROSTATE-SPECIFIC MEMBRANE ANTIGEN AND  
; NUMBER OF SEQUENCES: 48  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooper & Dunham LLP  
; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: United States of America  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM 330 466 DX2  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/394,152A  
; FILING DATE: 24-FEB-95  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White, John P.  
; REGISTRATION NUMBER: 28,678  
; REFERENCE/DOCKET NUMBER: 41426-B  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 278-0400  
; TELEFAX: (212) 391-0525  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2653 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; ORGANISM: Homo sapiens  
; TISSUE TYPE: Carcinoma  
; IMMEDIATE SOURCE:  
; CLONE: Prostate-Specific Membrane Antigen  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 262..2511  
US-08-394-152A-1

Query Match 100.0%; Score 27; DB 2; Length 2653;  
Best Local Similarity 100.0%; Pred. No. 0.00048;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 271 CTCCTTCACGAAACCGACTCGGCTGTG 297  
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RESULT 3  
US-08-394-152A-48/C  
; Sequence 48, Application US/08394152A  
; Patent No. 5935818  
; GENERAL INFORMATION:  
; APPLICANT: Israeli, Ron S.  
; APPLICANT: Heston, Warren D.W.  
; APPLICANT: Fair, William R.  
; TITLE OF INVENTION: PROSTATE-SPECIFIC MEMBRANE ANTIGEN AND  
; NUMBER OF SEQUENCES: 48  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooper & Dunham LLP  
; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: United States of America  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM 330 466 DX2  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/394,152A  
; FILING DATE: 24-FEB-95  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White, John P.  
; REGISTRATION NUMBER: 28,678  
; REFERENCE/DOCKET NUMBER: 41426-B  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 278-0400  
; TELEFAX: (212) 391-0525  
; INFORMATION FOR SEQ ID NO: 48:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2957 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; ORGANISM: Homo Sapien  
; TISSUE TYPE: Carcinoma  
; IMMEDIATE SOURCE:  
; CLONE: Prostate Specific Membrane Antigen  
US-08-394-152A-48  
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Best Local Similarity 100.0%; Pred. No. 0.00049;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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DB 263 CTCCTTCACGAAACCGACTCGGCTGTG 237

RESULT 4  
US-08-394-152A-39  
; Sequence 39, Application US/08394152A  
; Patent No. 5935818  
; GENERAL INFORMATION:  
; APPLICANT: Israeli, Ron S.  
; APPLICANT: Heston, Warren D.W.  
; APPLICANT: Fair, William R.  
; TITLE OF INVENTION: PROSTATE-SPECIFIC MEMBRANE ANTIGEN AND  
; NUMBER OF SEQUENCES: 48  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooper & Dunham LLP  
; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: United States of America  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM 330 466 DX2  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/394,152A  
; FILING DATE: 24-FEB-95  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White, John P.  
; REGISTRATION NUMBER: 28,678  
; REFERENCE/DOCKET NUMBER: 41426-B  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 278-0400  
; TELEFAX: (212) 391-0525  
; INFORMATION FOR SEQ ID NO: 48:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2957 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; ORGANISM: Homo Sapien  
; TISSUE TYPE: Carcinoma  
; IMMEDIATE SOURCE:  
; CLONE: Prostate Specific Membrane Antigen  
US-08-394-152A-48

GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: April 14, 2003, 13:13:08 ; Search time 33.6667 Seconds  
(without alignments)  
703.471 Million cell updates/sec

Title: US-09-821-734-12

Perfect score: 27

Sequence: 1 CTCCTTCACGAACCGACTCGGTGTG 27

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 593429 seqs, 438583690 residues

Total number of hits satisfying chosen parameters: 1186858

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications\_NA:\*

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- 3: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq:\*
- 4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq:\*
- 5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq:\*
- 6: /cgn2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq:\*
- 7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq:\*
- 8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq:\*
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- 10: /cgn2\_6/ptodata/1/pubpna/US09\_PUBCOMB.seq:\*
- 11: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq:\*
- 12: /cgn2\_6/ptodata/1/pubpna/US10\_PUBCOMB.seq:\*
- 13: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*
- 14: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
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2	27	100.0	101	10	US-09-925-300-900
3	27	100.0	866	10	US-09-925-300-131
4	27	100.0	2558	9	US-09-978-295A-617
5	27	100.0	2558	9	US-09-978-697-617
6	27	100.0	2558	9	US-09-978-192A-617
7	27	100.0	2558	9	US-09-999-832A-617
8	27	100.0	2558	9	US-09-978-189-617
9	27	100.0	2558	9	US-10-174-590-103
10	27	100.0	2558	9	US-10-175-737-103
11	27	100.0	2558	9	US-10-175-737-103
12	27	100.0	2558	9	US-10-173-706-103
13	27	100.0	2558	9	US-10-175-738-103
14	27	100.0	2558	9	US-10-175-752-103
15	27	100.0	2558	9	US-10-176-482-103
16	27	100.0	2558	9	US-10-176-757-103
17	27	100.0	2558	9	US-10-176-913-103
18	27	100.0	2558	9	US-10-180-552-103
19	27	100.0	2558	9	US-10-180-557-103

20	27	100.0	2558	9	US-10-173-700-103	Sequence 103, App
21	27	100.0	2558	9	US-10-174-572-103	Sequence 103, App
22	27	100.0	2558	9	US-10-174-579-103	Sequence 103, App
23	27	100.0	2558	9	US-10-174-582-103	Sequence 103, App
24	27	100.0	2558	9	US-10-174-588-103	Sequence 103, App
25	27	100.0	2558	9	US-10-175-739-103	Sequence 103, App
26	27	100.0	2558	9	US-10-175-740-103	Sequence 103, App
27	27	100.0	2558	9	US-10-176-488-103	Sequence 103, App
28	27	100.0	2558	9	US-10-176-492-103	Sequence 103, App
29	27	100.0	2558	9	US-10-176-492-103	Sequence 103, App
30	27	100.0	2558	9	US-10-176-747-103	Sequence 103, App
31	27	100.0	2558	9	US-10-176-750-103	Sequence 103, App
32	27	100.0	2558	9	US-10-176-985-103	Sequence 103, App
33	27	100.0	2558	9	US-10-176-987-103	Sequence 103, App
34	27	100.0	2558	9	US-10-176-991-103	Sequence 103, App
35	27	100.0	2558	9	US-10-176-992-103	Sequence 103, App
36	27	100.0	2558	9	US-10-176-993-103	Sequence 103, App
37	27	100.0	2558	9	US-10-184-658-103	Sequence 103, App
38	27	100.0	2558	9	US-10-173-695-103	Sequence 103, App
39	27	100.0	2558	9	US-10-173-697-103	Sequence 103, App
40	27	100.0	2558	9	US-10-173-705-103	Sequence 103, App
41	27	100.0	2558	9	US-10-174-576-103	Sequence 103, App
42	27	100.0	2558	9	US-10-174-585-103	Sequence 103, App
43	27	100.0	2558	9	US-10-174-586-103	Sequence 103, App
44	27	100.0	2558	9	US-10-175-747-103	Sequence 103, App
45	27	100.0	2558	9	US-10-176-481-103	Sequence 103, App

ALIGNMENTS

RESULT 1  
US-09-821-734-12  
; Sequence 12, Application US/09821734  
; Publication No. US20030027246A1  
; GENERAL INFORMATION:  
; APPLICANT: Chong, Pele  
; APPLICANT: Pedyczak, Artur  
; APPLICANT: Sia, Charles Dwo Yuan  
; TITLE OF INVENTION: Immunogenic Peptides Derived from Prostate-Specific Membrane  
; FILE REFERENCE: 11014-22  
; CURRENT APPLICATION NUMBER: US/09/821,734  
; PRIOR FILING DATE: 2001-03-30  
; PRIOR APPLICATION NUMBER: US 60/193,386  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 12  
; LENGTH: 27  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: CUP326  
US-09-821-734-12  
  
Query Match 100.0%; Score 27; DB 9; Length 27;  
Best Local Similarity 100.0%; Pred. No. 0.00034;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 CTCCTTCACGAACCGACTCGGTGTG 27  
DB 1 CTCCTTCACGAACCGACTCGGTGTG 27  
  
RESULT 2  
US-09-925-300-900  
; Sequence 900, Application US/09925300  
; Patent No. US20020151681A1  
; GENERAL INFORMATION:  
; APPLICANT: Craig Rosen,  
; APPLICANT: Steve Ruben  
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

FILE REFERENCE: PA101  
CURRENT APPLICATION NUMBER: US/09/925,300  
CURRENT FILING DATE: 2001-08-10  
PRIOR APPLICATION NUMBER: PCT/US00/05988  
PRIOR FILING DATE: 2000-03-08  
PRIOR APPLICATION NUMBER: 60/124,270  
PRIOR FILING DATE: 1999-03-12  
NUMBER OF SEQ ID NOS: 1890  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 900  
LENGTH: 101  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (29)  
OTHER INFORMATION: n equals a,t,g, or c  
NAME/KEY: misc feature  
LOCATION: (40)  
OTHER INFORMATION: n equals a,t,g, or c  
NAME/KEY: misc feature  
LOCATION: (54)  
OTHER INFORMATION: n equals a,t,g, or c  
NAME/KEY: misc feature  
LOCATION: (89)  
OTHER INFORMATION: n equals a,t,g, or c  
NAME/KEY: misc feature  
LOCATION: (99)  
OTHER INFORMATION: n equals a,t,g, or c  
US-09-925-300-900

Query Match 100.0%; Score 27; DB 10; Length 101;  
Best Local Similarity 100.0%; Pred. No. 0.00036;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCCTTCACGAACCGACTCGGCTGTG 27  
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Db 61 CTCCTTCACGAACCGACTCGGCTGTG 87

RESULT 3  
US-09-925-300-131  
Sequence 131, Application US/09925300  
Patent No. US20020151681A1  
GENERAL INFORMATION:  
APPLICANT: Craig Rosen,  
APPLICANT: Steve Ruben  
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
FILE REFERENCE: PA101  
CURRENT APPLICATION NUMBER: US/09/925,300  
CURRENT FILING DATE: 2001-08-10  
PRIOR APPLICATION NUMBER: PCT/US00/05988  
PRIOR FILING DATE: 2000-03-08  
PRIOR APPLICATION NUMBER: 60/124,270  
PRIOR FILING DATE: 1999-03-12  
NUMBER OF SEQ ID NOS: 1890  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 131  
LENGTH: 866  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (683)  
OTHER INFORMATION: n equals a,t,g, or c  
NAME/KEY: misc feature  
LOCATION: (723)  
OTHER INFORMATION: n equals a,t,g, or c  
NAME/KEY: misc feature  
LOCATION: (740)  
OTHER INFORMATION: n equals a,t,g, or c  
NAME/KEY: misc feature  
LOCATION: (793)

OTHER INFORMATION: n equals a,t,g, or c  
NAME/KEY: misc feature  
LOCATION: (813)  
OTHER INFORMATION: n equals a,t,g, or c  
NAME/KEY: misc feature  
LOCATION: (841)  
OTHER INFORMATION: n equals a,t,g, or c  
US-09-925-300-131

Query Match 100.0%; Score 27; DB 10; Length 866;  
Best Local Similarity 100.0%; Pred. No. 0.00041;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 220 CTCCTTCACGAACCGACTCGGCTGTG 246

RESULT 4  
US-09-978-295A-617  
Sequence 617, Application US/09978295A  
Patent No. US20020156006A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
Acids Encoding the Same  
FILE REFERENCE: P2630P1C11  
CURRENT APPLICATION NUMBER: US/09/978,295A  
CURRENT FILING DATE: 2001-10-15  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/064249  
PRIOR FILING DATE: 1997-11-03  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066364  
PRIOR FILING DATE: 1997-11-21  
PRIOR APPLICATION NUMBER: 60/077450  
PRIOR FILING DATE: 1998-03-10  
PRIOR APPLICATION NUMBER: 60/077632  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077641  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077649  
PRIOR FILING DATE: 1998-03-11



GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: April 14, 2003, 09:33:49 ; Search time 828.5 seconds  
(without alignments)  
527.795 Million cell updates/sec

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Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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  - 2: em\_esthum:\*\*
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  - 4: em\_estmu:\*\*
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  - 6: em\_estpi:\*\*
  - 7: em\_estro:\*\*
  - 8: em\_htc:\*\*
  - 9: gb\_est1:\*\*
  - 10: gb\_est2:\*\*
  - 11: gb\_hic:\*\*
  - 12: gb\_est3:\*\*
  - 13: gb\_est4:\*\*
  - 14: gb\_est5:\*\*
  - 15: em\_estfun:\*\*
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  - 17: gb\_gss:\*\*
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  - 21: em\_gss\_vrt:\*\*
  - 22: em\_gss\_fun:\*\*
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  - 24: em\_gss\_mus:\*\*
  - 25: em\_gss\_other:\*\*
  - 26: em\_gss\_pro:\*\*
  - 27: em\_gss\_rod:\*\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	27	100.0	484	17	AQ636441	AQ636441 RPC1-11-4
5	27	100.0	704	13	BI772735	BI772735 603053273
6	27	100.0	882	14	BQ708386	BQ708386 AGENCOURT

7	27	100.0	902	14	BQ708480	BQ708480 AGENCOURT	
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10	27	100.0	917	14	BQ711571	BQ711571 AGENCOURT	
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13	27	100.0	998	14	BQ711650	BQ711650 AGENCOURT	
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17	20.2	74.8	539	13	BJ040403	BJ040403	
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23	18.6	68.9	474	10	BB807530	BB807530	
c	24	18.6	68.9	507	9	AA530080	AA530080 vj37b01.r
25	18.6	68.9	515	9	AA261631	AA261631 mz87c12.r	
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c	27	18.6	68.9	683	14	BQ444546	BQ444546 UI-M-ER0-
28	18.6	68.9	788	12	BG069703	BG069703 H3079B12-	
c	29	18.6	68.9	1289	12	BF670658	BF670658 602149893
c	30	18.6	68.9	1701	11	AK008165	AK008165 Mus muscu
c	31	18.6	68.9	2043	11	BC016206	BC016206 Mus muscu
c	32	18.6	68.9	2077	11	BC025124	BC025124 Mus muscu
c	33	18.2	67.4	409	14	R67855	R67855 y128d11.s1
c	34	18.2	67.4	879	14	BQ429613	BQ429613 AGENCOURT
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36	18	66.7	290	10	BB099715	BB099715	
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ALIGNMENTS

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ACCESSION	AV692993	405 bp	mRNA	linear	EST 16-JAN-2002
VERSION	AV692993.1	405 bp	mRNA	linear	EST 16-JAN-2002
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SOURCE	human	405 bp	mRNA	linear	EST 16-JAN-2002
ORGANISM	Homo sapiens	405 bp	mRNA	linear	EST 16-JAN-2002
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	405 bp	mRNA	linear	EST 16-JAN-2002
AUTHORS	Xu,X., Huang,J., Xu,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X., Xiao,H., Qu,J., Liu,F., Huang,Q., Cheng,Z., Li,N., Du,J., Hu,W., Shen,K., Lu,G., Fu,G., Zhong,M., Xu,S., Gu,W., Huang,W., Zhao,X., Hu,G., Gu,J., Chen,Z. and Han,Z.	405 bp	mRNA	linear	EST 16-JAN-2002
TITLE	Insight into hepatocellular carcinogenesis at transcriptome level by comparing gene expression profiles of hepatocellular carcinoma with those of corresponding noncancerous liver	405 bp	mRNA	linear	EST 16-JAN-2002
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)	405 bp	mRNA	linear	EST 16-JAN-2002
MEDLINE	21625106	405 bp	mRNA	linear	EST 16-JAN-2002
COMMENT	Contact: Zequang Han Chinese National Human Genome Center at Shanghai 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai 201203, P. R. China Tel: 86-21-50801919(ex.45) Fax: 86-21-50801922 Email: hanzg@chgc.sh.cn This clone is available at CHGC in Shanghai.	405 bp	mRNA	linear	EST 16-JAN-2002

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Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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LOCUS
DEFINITION
CM0-NN0079-140400-334-f10 NN0079 Homo sapiens cDNA, mRNA sequence.
ACCESSION
AW898913.1 GI:8063118
VERSION
AW898913.1 GI:8063118
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 420)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tbl=st2=CM0-NN0079-140
400-334-f10&st3=2000-04-14&st4=1)
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High quality sequence stop: 420.
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Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
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Db 135 CTCCTTCACGAAACCGACTCGGCTGTG 161
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RESULT 4
AQ636441
LOCUS
DEFINITION
RPCI-11-477N9.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-477N9,
DNA sequence.
ACCESSION
AQ636441
VERSION
AQ636441.1 GI:50999076

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GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model  
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(without alignments)  
1500.527 Million cell updates/sec

Title: US-09-821-734-13  
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Gapop 10.0 , Gapext 1.0

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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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6: gb.pat.\*  
7: gb.ph.\*  
8: gb.pl.\*  
9: gb.pr.\*  
10: gb.ro.\*  
11: gb.sts.\*  
12: gb.sy.\*  
13: gb.un.\*  
14: gb.vi.\*  
15: em.ba.\*  
16: em.fun.\*  
17: em.hum.\*  
18: em.in.\*  
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37: em.htg\_vrt.\*  
38: em\_sy.\*  
39: em.htgo\_hum.\*  
40: em.htgo\_mus.\*  
41: em.htgo\_other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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5	27	100.0	198	9	AF016826	U93599 Homo sapien
6	27	100.0	444	11	G53000	G53000 SHGC-81785
7	27	100.0	1641	9	AF107214	AF107214 Homo sapi
8	27	100.0	2253	6	AX467227	AX467227 Sequence
9	27	100.0	2253	9	AY101595	AY101595 Homo sapi
10	27	100.0	2472	9	BC025672	BC025672 Homo sapi
11	27	100.0	2518	9	AF176574	AF176574 Homo sapi
12	27	100.0	2558	6	AX376036	AX376036 Sequence
13	27	100.0	2653	6	AX337498	AX337498 Sequence
14	27	100.0	2653	6	I23794	I23794 Sequence 1
15	27	100.0	2653	9	HUMPSM	M99487 Human prost
16	27	100.0	93523	9	AF007544	AF007544 Homo sapi
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18	27	100.0	129095	9	AC110742	AC110742 Homo sapi
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22	23	85.2	592	9	HS47318	AJ007318 Homo sapi
23	20.6	76.3	103656	10	AL713958	AL713958 Mouse DNA
24	20.6	76.3	237588	2	AC025581	AC025581 Mus muscu
25	20.2	74.8	134725	2	AC109418	AC109418 Rattus no
26	20.2	74.8	151453	2	AC118988	AC118988 Sus scrof
27	20.2	74.8	173168	2	AC114035	AC114035 Rattus no
28	20.2	74.8	202748	10	MM0307670	AJ307670 Mus muscu
29	20.2	74.8	217073	2	AC094162	AC094162 Rattus no
30	20.2	74.8	237181	2	AC126441	AC126441 Mus muscu
31	19.8	73.3	171787	2	AC126967	AC126967 Rattus no
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36	19.6	72.6	111117	2	AC097920	AC097920 Rattus no
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38	19.6	72.6	157192	2	AP005395	AP005395 Oryza sat
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ALIGNMENTS

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DEFINITION Sequence 13 from Patent WO0174845.  
ACCESSION AX268375  
VERSION AX268375.1 GI:16541582  
KEYWORDS synthetic construct.  
SOURCE synthetic construct.  
ORGANISM artificial sequences.  
REFERENCE 1  
AUTHORS pedyczak, A., Chong, F. and Sia, C.D.  
TITLE Immunogenic peptides derived from prostate-specific membrane  
antigen (psma) and uses thereof  
JOURNAL Patent: WO 01/74845-A 13 11-OCT-2001;

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LOCUS AR077260 72 bp DNA linear PAT 31-AUG-2000
DEFINITION Sequence 1 from patent US 5962237.
ACCESSION AR077260
VERSION AR077260.1 GI:10004006
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 72)
AUTHORS Ts'o,P.O.P., Wang,Z.-P., Leek,S.A., Nelson,W.G. and Partin,A.W.
TITLE Method of enriching rare cells
JOURNAL Patent: US 5962237-A 1 05-OCT-1999;
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LOCUS AF008934 127 bp DNA linear STS 16-SEP-1997
DEFINITION Homo sapiens prostate-specific membrane antigen related sequence,
sequence tagged site.
ACCESSION AF008934
VERSION AF008934.1 GI:2393914
KEYWORDS STS.
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE 1 (bases 1 to 127)
JOURNAL Prostate-Specific Membrane Antigen Related Gene
REFERENCE 2 (bases 1 to 127)
AUTHORS Maraj,B.H., Whelan,P. and Markham,A.F.
TITLE Direct Submission
JOURNAL Submitted (17-JUN-1997) Molecular Medicine Unit, Leeds University,
Beckett, Leeds, Yorkshire LS9 7TF, England
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DEFINITION Homo sapiens prostate specific-membrane antigen gene, exon 1.
ACCESSION AF016826
VERSION AF016826.1 GI:2335203
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE 1 (bases 1 to 129)
JOURNAL Detailed genetic mapping around a putative prostate-specific
membrane antigen locus on human chromosome 11p11.2
FEATURES Location/Qualifiers
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RESULT 4
LOCUS HSU93599 129 bp DNA linear PRI 05-JUL-2001
DEFINITION Homo sapiens PSM pseudogene, partial sequence.
ACCESSION U93599
VERSION U93599.1 GI:1928993
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE 1 (bases 1 to 129)
AUTHORS Maraj,B.H., Leek,J.P., Karayi,M., Ali,M., Lench,N.J. and
Markham,A.F.
TITLE Detailed genetic mapping around a putative prostate-specific
membrane antigen locus on human chromosome 11p11.2
JOURNAL Cytogenet. Cell Genet. 81 (1), 3-9 (1998)
FEATURES Location/Qualifiers
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    /db_xref="taxon:9606"
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    /map="llql4"
    /gene="PSM"
    /pseudo
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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 77 GTGCTGGCGGTGGCTTCCTTCCTC 103

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    subpanel"
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    /note="similar to prostate-specific membrane antigen gene"
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ORIGIN
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GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model.

Run on: April 14, 2003, 09:27:29 ; Search time 99 seconds  
(without alignments)  
614.181 Million cell updates/sec

Title: US-09-821-734-13

Perfect score: 27

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Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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23: /SID22/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.\*  
24: /SID22/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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1	27	100.0	27	22	AA15140 Human DNA encoding
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3	27	100.0	866	21	AA15696 Human prostate can
4	27	100.0	2253	21	AA109454 Human prostate spe
5	27	100.0	2558	21	AA178599 Human PRO739 nucle
6	27	100.0	2558	22	AA145976 Human DNA encoding
7	27	100.0	2653	15	AA165520 Prostate-specific
8	27	100.0	2653	24	ABK86204 cDNA encoding huma
9	27	100.0	2653	24	ABK64556 Human benign prost

10	27	100.0	2653	24	ABL69670	Prostate cancer re
11	27	100.0	2654	17	AA136785	Prostate-specific
12	27	100.0	2884	23	ABV22873	Human prostate exp
13	27	100.0	2884	23	ABV23013	Human prostate exp
14	27	100.0	2884	23	ABV28703	Human prostate exp
15	27	100.0	2884	23	ABV28849	Human prostate exp
16	27	100.0	3017	17	AA136776	Prostate-specific
17	27	100.0	3017	17	AA136786	Prostate-specific
18	21.2	78.5	687	24	ABQ91413	M. capsulatus gene
19	19.6	72.6	462	24	ABK79735	Bacillus clausii g
20	19	70.4	5090	19	AAV53575	Nucleotide sequenc
21	18.6	68.9	3261	23	ABL16703	Drosophila melanog
22	18.6	68.9	3261	23	AA189027	DNA encoding novel
23	18.6	68.9	12216	23	ABL16702	Drosophila melanog
24	18.2	67.4	713	23	ABL13269	Drosophila melanog
25	18.2	67.4	3144	23	ABL13268	Drosophila melanog
26	18.2	67.4	3914	23	ABL12804	Drosophila melanog
27	18	66.7	459	19	AAV31291	E. coli J96 pathog
28	18	66.7	678	24	ABT03011	Human breast speci
29	18	66.7	1388	21	AA149992	Arabidopsis thalia
30	18	66.7	1390	21	AA136747	Arabidopsis thalia
31	18	66.7	1470	17	AA130650	P. gingivalis haem
32	18	66.7	1470	19	AAV58871	Haemagglutinin pro
33	18	66.7	1841	17	AA130651	P. gingivalis haem
34	18	66.7	1841	19	AAV58872	Haemagglutinin pro
35	18	66.7	1872	21	AA105527	Streptococcus pneu
36	18	66.7	3472	23	AA172696	DNA encoding novel
37	18	66.7	10004	22	AB144483	Human nervous syst
38	18	66.7	10246	22	AB144485	Human nervous syst
39	18	66.7	10254	19	AAV52162	Streptococcus pneu
40	18	66.7	10732	21	AA105594	Gene encoding a su
41	17.8	65.9	2297	21	AA193309	Sequence encoding
42	17.6	65.2	148	21	AA124222	Human secreted pro
43	17.6	65.2	175	21	AA12195	Human secreted pro
44	17.6	65.2	240	21	AA12713	Human secreted pro
45	17.6	65.2	265	22	AA180499	Human polynucleoti

#### ALIGNMENTS

RESULT 1  
AA15140  
ID AA15140 standard; DNA; 27 BP.

XX AA15140;

DT 16-JAN-2002 (first entry)

XX Human DNA encoding a PSMA derived immunogenic peptide CLP328.

XX Human; ds; PSMA; prostate specific membrane antigen; prostate cancer;  
KW tumour; immunogenic peptide; cytostatic; gene therapy; CLP328.

XX Homo sapiens.

XX Key Location/Qualifiers

FT CDS 1..27

FT /\*tag= a

FT /product= "CLP328"

FT /partial

FT /note= "No start or stop codon"

XX WO200174845-A2.

XX 11-OCT-2001.

XX 30-MAR-2001; 2001WO-CA00411.

XX 31-MAR-2000; 2000US-193386P.

XX (AVET ) AVENTIS PASTEUR LTD.

XX

```

PI Pedyczak A, Chong P, Sia CDY;
XX WPI: 2001-626378/72.
XX P-PSDB; AAU09105.
XX
XX New polypeptides useful for inducing an immune response and treating
XX prostate cancer comprises polypeptides derived from the prostate
XX specific membrane antigen -
XX
XX Claim 6; Page 15; 47pp; English.
XX
XX The invention relates to prostate specific membrane antigen (PSMA)
XX derived peptides (and the nucleic acids encoding them) capable of
XX eliciting an immune response. The molecules of the invention are used to
XX elicit an immune response, particularly to treat cancer and tumours,
XX especially prostate cancer. Delivery of the peptides may be by
XX expression from the nucleic acids encoding them (i.e. gene therapy).
XX The present sequence encodes a PSMA derived immunogenic peptide.
XX
XX Sequence 27 BP; 0 A; 8 C; 9 G; 10 T; 0 other;
XX
Query Match 100.0%; Score 27; DB 22; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.051;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GTGCTGGCGGTGGCTTCTTCTCCTC 27
Db 1 GTGCTGGCGGTGGCTTCTTCTCCTC 27
RESULT 2
AAT89210
ID AAT89210 standard; DNA; 72 BP.
XX
XX AAT89210;
XX
XX 30-APR-1998 (first entry)
XX
XX Prostate specific membrane antigen mRNA probe 1.
XX
XX Prostate specific membrane antigen; PSMA; probe; hybridisation:
XX cancer; vaccine; ss.
XX
XX Synthetic.
XX Homo sapiens.
XX
XX WO9738313-A1.
XX
XX 16-OCT-1997.
XX
XX 02-APR-1997; 97WO-US05586.
XX
XX 05-APR-1996; 96US-0014929.
XX
XX (UXJO ) UNIV JOHNS HOPKINS.
XX
XX Lesko SA, Nelson WG, Partin AW, Tso POP, Wang Z;
XX WPI: 1997-512878/47.
XX
XX Isolating rare cells by density gradient separation then negative
XX selection - used for enriching prostatic cancer cells for diagnosis,
XX staging and monitoring of disease
XX
XX Claim 12; Page 21; 63pp; English.
XX
XX This sequence is a probe for prostate specific membrane antigen (PSMA),
XX particularly useful for in situ hybridisation. The probe is used to
XX detect the epithelial cells of prostatic cancer cells, via the
XX detection of PSA (prostate specific antigen) and/or PSMA. The method
XX is especially used to enrich prostatic cancer cells from blood,
XX allowing detection and characterisation of these cells for diagnosis,
XX staging and monitoring of disease. It can also be applied to the

```

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```

CC enrichment of liver, hepatoma, hepatocarcinoma or cancer cells in
CC general.
XX
XX Sequence 72 BP; 2 A; 18 C; 27 G; 25 T; 0 other;
XX
Query Match 100.0%; Score 27; DB 18; Length 72;
Best Local Similarity 100.0%; Pred. No. 0.056;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GTGCTGGCGGTGGCTTCTTCTCCTC 27
Db 22 GTGCTGGCGGTGGCTTCTTCTCCTC 48
RESULT 3
AAF15696
ID AAF15696 standard; cDNA; 866 BP.
XX
XX AAF15696;
XX
XX 13-MAR-2001 (first entry)
XX
XX Human prostate cancer antigen nucleotide sequence SEQ ID NO:131.
XX
XX Human; prostate cancer; prostate cancer antigen; detection; diagnosis;
XX neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular;
XX vulnary; gastrointestinal; nephrotropic; antiinfective; gynaecological;
XX antibacterial; gene therapy; neural; immune; reproductive; renal;
XX gastrointestinal; pulmonary; cardiovascular; proliferative disorder;
XX wound; infectious disease; ss.
XX
XX Homo sapiens.
XX
XX WO2000055174-A1.
XX
XX 21-SEP-2000.
XX
XX 08-MAR-2000; 2000WO-US05988.
XX
XX 12-MAR-1999; 99US-01242770.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX (ROSE/) ROSEN C.A.
XX
XX Rosen CA, Ruben SM;
XX
XX WPI: 2000-587513/55.
XX P-PSDB; AAB56493.
XX
XX Prostate cancer associated gene sequences, referred to as prostate
XX cancer antigens, useful for treatment, prevention, and diagnosis of
XX disorders such as prostate cancer -
XX
XX Claim 1; Page 697-698; 2338pp; English.
XX
XX AAF15566 to AAF16505 encode the human prostate cancer associated
XX proteins, called prostate cancer antigens, given in AAB56363 to AAB57302.
XX The prostate cancer antigens can have neuroprotective, cytostatic,
XX cardioactive, immunomodulatory, muscular, vulnary, gastrointestinal,
XX nephrotropic, antiinfective, gynaecological and antibacterial activities,
XX and can be used in gene therapy. The prostate cancer antigen
XX polynucleotides may be used for detection of prostate cancer,
XX identification, as chromosome markers, and for numerous other diagnostic
XX or research purposes. The prostate cancer antigens may be used to treat
XX disorders such as neural, immune, muscular, reproductive,
XX gastrointestinal, pulmonary, cardiovascular, renal, and proliferative
XX disorders, wounds, and infectious diseases. AAF16506 to AAF16514 to
XX AAB57303 represent sequences used in the exemplification of the present
XX invention.
XX
XX Sequence 866 BP; 236 A; 193 C; 213 G; 215 T; 9 other;
XX
Query Match 100.0%; Score 27; DB 21; Length 866;

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GenCore version 5.1.3  
Copyright (c) 1993 - 2003 Compugen Ltd.

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Run on: April 14, 2003, 10:10:25 ; Search time 21 Seconds  
(without alignments)  
394.299 Million cell updates/sec

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Total number of hits satisfying chosen parameters: 882724

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	27	100.0	2653	1	US-08-325-553-1	Sequence 1, Appli
3	27	100.0	2853	2	US-08-394-152A-1	Sequence 1, Appli
c 4	27	100.0	2957	2	US-08-394-152A-48	Sequence 48, Appl
5	27	100.0	3017	2	US-08-394-152A-39	Sequence 39, Appl
c 6	18	66.7	459	4	US-08-976-259-105	Sequence 105, App
c 7	18	66.7	1265	4	US-09-221-017B-566	Sequence 566, App
c 8	18	66.7	1470	1	US-08-570-311-3	Sequence 3, Appli
c 9	18	66.7	1470	2	US-08-353-485-3	Sequence 3, Appli
c 10	18	66.7	1841	1	US-08-570-311-5	Sequence 5, Appli
c 11	18	66.7	1841	2	US-08-353-485-5	Sequence 5, Appli
c 12	18	66.7	10254	4	US-08-961-527-29	Sequence 29, Appl
13	17.4	64.4	522	2	US-08-768-964-14	Sequence 14, Appl
c 14	17.4	64.4	522	2	US-08-768-964-15	Sequence 15, Appl
c 15	17.4	64.4	522	3	US-09-005-299-14	Sequence 14, Appl
c 16	17.4	64.4	522	3	US-09-005-299-15	Sequence 15, Appl
17	17.4	64.4	522	4	US-09-515-431-14	Sequence 14, Appl
c 18	17.4	64.4	522	4	US-09-515-431-15	Sequence 15, Appl
c 19	17.4	64.4	590	1	US-08-580-038-15	Sequence 15, Appl
20	17.4	64.4	591	1	US-08-580-038-5	Sequence 5, Appli
21	17.4	64.4	591	1	US-08-580-038-12	Sequence 12, Appl
22	17.4	64.4	592	1	US-08-580-038-19	Sequence 19, Appl
23	17.4	64.4	597	2	US-08-768-964-11	Sequence 11, Appl
c 24	17.4	64.4	597	2	US-08-768-964-16	Sequence 16, Appl
25	17.4	64.4	597	3	US-09-005-299-11	Sequence 11, Appl
c 26	17.4	64.4	597	3	US-09-005-299-16	Sequence 16, Appl
27	17.4	64.4	597	4	US-09-515-431-11	Sequence 11, Appl

c 28	17.4	64.4	597	4	US-09-515-431-16	Sequence 16, Appl
29	17.4	64.4	633	1	US-08-580-038-84	Sequence 84, Appl
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c 31	17.4	64.4	714	2	US-08-768-964-8	Sequence 8, Appli
32	17.4	64.4	714	3	US-09-005-299-6	Sequence 6, Appli
c 33	17.4	64.4	714	3	US-09-005-299-8	Sequence 8, Appli
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c 38	17.4	64.4	789	3	US-09-005-299-4	Sequence 4, Appli
c 39	17.4	64.4	789	3	US-09-005-299-5	Sequence 5, Appli
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c 41	17.4	64.4	789	4	US-09-515-431-5	Sequence 5, Appli
c 42	17.4	64.4	1069	2	US-08-768-964-1	Sequence 1, Appli
c 43	17.4	64.4	1069	2	US-08-768-964-3	Sequence 3, Appli
c 44	17.4	64.4	1069	3	US-09-005-299-1	Sequence 1, Appli
c 45	17.4	64.4	1069	3	US-09-005-299-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1  
US-08-832-468-1  
; Sequence 1, Application US/08832468  
; Patent No. 5952237  
; GENERAL INFORMATION:  
; APPLICANT: TS O, Paul O.P.  
; APPLICANT: Wang, Zheng-Pin  
; APPLICANT: Lesko, Stephen A.  
; APPLICANT: Nelson, William G.  
; APPLICANT: Partin, Alan W.  
; TITLE OF INVENTION: A METHOD OF ENRICHING RARE CELLS  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Leydig, Voit & Mayer, Ltd.  
; STREET: 700 Thirteenth St., NW  
; CITY: Washington  
; STATE: DC  
; COUNTRY: US  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
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; APPLICATION NUMBER: US/08/832,468  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60-014929  
; FILING DATE: 05-APR-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Jay, Jeremy M.  
; REGISTRATION NUMBER: 33587  
; REFERENCE/DOCKET NUMBER: 72466  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-737-6770  
; TELEFAX: 202-737-6776  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 72 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: other nucleic acid (synthetic DNA)  
US-08-832-468-1  
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Best Local Similarity 100.0%; Pred. No. 0.0047;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGCTGGCGGTGGCTTCTTCTCCTC 27  
Db 22 GTGCTGGCGGTGGCTTCTTCTCCTC 48

## RESULT 2

US-08-325-553-1

; Sequence 1, Application US/08325553  
; Patent No. 5538866

; GENERAL INFORMATION:

; APPLICANT: Israeli, Ron S.

; APPLICANT: Heston, Warren D.W.

; APPLICANT: Fair, William R.

; TITLE OF INVENTION: THE PROSTATE-SPECIFIC MEMBRANE ANTIGEN

; NUMBER OF SEQUENCES: 38

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Cooper & Dunham

; STREET: 30 Rockefeller Plaza

; CITY: New York

; STATE: New York

; COUNTRY: United States of America

; ZIP: 10112

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/325,553

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/07/973,337A

; FILING DATE: 05 NOV 1992

; ATTORNEY/AGENT INFORMATION:

; NAME: White, John P.

; REGISTRATION NUMBER: 28,678

; REFERENCE/DOCKET NUMBER: 1747/41426

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 977-9550

; TELEX: 422523 COOP UI

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 2653 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; ORIGINAL SOURCE:

; ORGANISM: Homo sapiens

; TISSUE TYPE: Carcinoma

; IMMEDIATE SOURCE:

; CLONE: Prostate-Specific Membrane Antigen

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 262..2511

; US-08-325-553-1

Query Match 100.0%; Score 27; DB 1; Length 2653;

Best Local Similarity 100.0%; Pred. No. 0.0074;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGCTGGCGGTGGCTTCTTCTCCTC 27

Db 340 GTGCTGGCGGTGGCTTCTTCTCCTC 366

## RESULT 3

US-08-394-152A-1

; Sequence 1, Application US/08394152A

; Patent No. 5935818

; GENERAL INFORMATION:

; APPLICANT: Israeli, Ron S.

; APPLICANT: Heston, Warren D.W.

; APPLICANT: Fair, William R.

; TITLE OF INVENTION: PROSTATE-SPECIFIC MEMBRANE ANTIGEN AND

; NUMBER OF SEQUENCES: 48

; CORRESPONDENCE ADDRESS:

; STREET: 1185 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: United States of America

; ZIP: 10036

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM 330 466 DX2

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/394,152A

; FILING DATE: 24-FEB-95

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: White, John P.

; REGISTRATION NUMBER: 28,678

; REFERENCE/DOCKET NUMBER: 41426-B

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 278-0400

; TELEFAX: (212) 391-0525

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 2653 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; ORIGINAL SOURCE:

; ORGANISM: Homo sapiens

; TISSUE TYPE: Carcinoma

; IMMEDIATE SOURCE:

; CLONE: Prostate-Specific Membrane Antigen

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 262..2511

; US-08-394-152A-1

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Best Local Similarity 100.0%; Pred. No. 0.0074;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGCTGGCGGTGGCTTCTTCTCCTC 27

Db 340 GTGCTGGCGGTGGCTTCTTCTCCTC 366

## RESULT 4

US-08-394-152A-48/C

; Sequence 48, Application US/08394152A

; Patent No. 5935818

; GENERAL INFORMATION:

; APPLICANT: Israeli, Ron S.

; APPLICANT: Heston, Warren D.W.

; APPLICANT: Fair, William R.

; TITLE OF INVENTION: PROSTATE-SPECIFIC MEMBRANE ANTIGEN AND

; NUMBER OF SEQUENCES: 48

; CORRESPONDENCE ADDRESS:

; STREET: 1185 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: United States of America

; ZIP: 10036

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM 330 466 DX2

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/394,152A

; FILING DATE: 24-FEB-95

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: White, John P.

; REGISTRATION NUMBER: 28,678

; REFERENCE/DOCKET NUMBER: 41426-B

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 278-0400

; TELEFAX: (212) 391-0525

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 2653 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; ORIGINAL SOURCE:

; ORGANISM: Homo sapiens

; TISSUE TYPE: Carcinoma

; IMMEDIATE SOURCE:

; CLONE: Prostate-Specific Membrane Antigen

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 262..2511

; US-08-394-152A-1



GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 14, 2003, 13:13:08 ; Search time 33.6667 Seconds  
(without alignments)  
703.471 Million cell updates/sec

Title: US-09-821-734-13

Perfect score: 27

Sequence: 1 gtgctggcgggtggtcttcttcctc 27

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 593429 seqs, 438583890 residues

Total number of hits satisfying chosen parameters: 1186858

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Published\_Applications\_NA.\*

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- 14: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	27	100.0	866	10	US-09-925-300-131
3	27	100.0	2558	9	US-09-978-295A-617
4	27	100.0	2558	9	US-09-978-697-617
5	27	100.0	2558	9	US-09-978-192A-617
6	27	100.0	2558	9	US-09-998-832A-617
7	27	100.0	2558	9	US-09-978-189-617
8	27	100.0	2558	9	US-10-174-590-103
9	27	100.0	2558	9	US-10-176-758-103
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13	27	100.0	2558	9	US-10-175-752-103
14	27	100.0	2558	9	US-10-176-482-103
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17	27	100.0	2558	9	US-10-180-552-103
18	27	100.0	2558	9	US-10-180-557-103
19	27	100.0	2558	9	US-10-173-700-103

20	27	100.0	2558	9	US-10-174-572-103	Sequence 103, App
21	27	100.0	2558	9	US-10-174-579-103	Sequence 103, App
22	27	100.0	2558	9	US-10-174-582-103	Sequence 103, App
23	27	100.0	2558	9	US-10-174-588-103	Sequence 103, App
24	27	100.0	2558	9	US-10-175-739-103	Sequence 103, App
25	27	100.0	2558	9	US-10-175-740-103	Sequence 103, App
26	27	100.0	2558	9	US-10-175-743-103	Sequence 103, App
27	27	100.0	2558	9	US-10-176-488-103	Sequence 103, App
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29	27	100.0	2558	9	US-10-176-747-103	Sequence 103, App
30	27	100.0	2558	9	US-10-176-750-103	Sequence 103, App
31	27	100.0	2558	9	US-10-176-985-103	Sequence 103, App
32	27	100.0	2558	9	US-10-176-987-103	Sequence 103, App
33	27	100.0	2558	9	US-10-176-991-103	Sequence 103, App
34	27	100.0	2558	9	US-10-176-992-103	Sequence 103, App
35	27	100.0	2558	9	US-10-176-993-103	Sequence 103, App
36	27	100.0	2558	9	US-10-184-658-103	Sequence 103, App
37	27	100.0	2558	9	US-10-173-695-103	Sequence 103, App
38	27	100.0	2558	9	US-10-173-697-103	Sequence 103, App
39	27	100.0	2558	9	US-10-173-705-103	Sequence 103, App
40	27	100.0	2558	9	US-10-174-576-103	Sequence 103, App
41	27	100.0	2558	9	US-10-174-585-103	Sequence 103, App
42	27	100.0	2558	9	US-10-174-586-103	Sequence 103, App
43	27	100.0	2558	9	US-10-175-747-103	Sequence 103, App
44	27	100.0	2558	9	US-10-176-481-103	Sequence 103, App
45	27	100.0	2558	9	US-10-176-485-103	Sequence 103, App

ALIGNMENTS

RESULT 1  
US-09-821-734-13  
; Sequence 13, Application US/09821734  
; Publication No. US20030027246A1  
; GENERAL INFORMATION:  
; APPLICANT: Chong, Pele  
; APPLICANT: Pedyczak, Artur  
; APPLICANT: Sia, Charles Dwo Yuan  
; TITLE OF INVENTION: Immunogenic Peptides Derived from Prostate-Specific Membrane  
; TITLE OF INVENTION: (PSMA) and Uses Thereof  
; FILE REFERENCE: 11014-22  
; CURRENT APPLICATION NUMBER: US/09/821,734  
; CURRENT FILING DATE: 2001-03-30  
; PRIOR APPLICATION NUMBER: US 60/193,386  
; PRIOR FILING DATE: 2000-03-31  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 13  
; LENGTH: 27  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: CUP328  
US-09-821-734-13

Query Match 100.0%; Score 27; DB 9; Length 27;  
Best Local Similarity 100.0%; Pred. No. 0.011;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGCTGGCGGGTGGCTTCTTCTCTC 27  
|||||  
DB 1 GTGCTGGCGGGTGGCTTCTTCTCTC 27

RESULT 2  
US-09-925-300-131  
; Sequence 131, Application US/09925300  
; Patent No. US20020151681A1  
; GENERAL INFORMATION:  
; APPLICANT: Craig Rosen,  
; APPLICANT: Steve Ruben  
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

FILE REFERENCE: PA101  
CURRENT APPLICATION NUMBER: US/09/925,300  
CURRENT FILING DATE: 2001-08-10  
PRIOR APPLICATION NUMBER: PCT/US00/05988  
PRIOR FILING DATE: 2000-03-08  
PRIOR APPLICATION NUMBER: 60/124,270  
PRIOR FILING DATE: 1999-03-12  
NUMBER OF SEQ ID NOS: 1890  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 131  
LENGTH: 866  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (683)  
OTHER INFORMATION: n equals a,t,g, or c  
NAME/KEY: misc feature  
LOCATION: (723)  
OTHER INFORMATION: n equals a,t,g, or c  
NAME/KEY: misc feature  
LOCATION: (740)  
OTHER INFORMATION: n equals a,t,g, or c  
NAME/KEY: misc feature  
LOCATION: (793)  
OTHER INFORMATION: n equals a,t,g, or c  
NAME/KEY: misc feature  
LOCATION: (813)  
OTHER INFORMATION: n equals a,t,g, or c  
NAME/KEY: misc feature  
LOCATION: (841)  
OTHER INFORMATION: n equals a,t,g, or c  
US-09-925-300-131

Query Match 100.0%; Score 27; DB 10; Length 866;  
Best Local Similarity 100.0%; Pred. No. 0.01;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 289 GTGCTGGCGGTCTTCTCTCTC 315

## RESULT 3

US-09-978-295A-617  
Sequence 617, Application US/09978295A  
Patent No. US20020156006A1

## GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnovers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Geritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel

APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630P1C11  
CURRENT APPLICATION NUMBER: US/09/978,295A  
CURRENT FILING DATE: 2001-10-15  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/064249  
PRIOR FILING DATE: 1997-11-03  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066364  
PRIOR FILING DATE: 1997-11-21  
PRIOR APPLICATION NUMBER: 60/077450  
PRIOR FILING DATE: 1998-03-10  
PRIOR APPLICATION NUMBER: 60/077632  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077641  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077649  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077791  
PRIOR FILING DATE: 1998-03-12  
PRIOR APPLICATION NUMBER: 60/078004  
PRIOR FILING DATE: 1998-03-13  
PRIOR APPLICATION NUMBER: 60/078886  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/078936  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/078910  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/078939  
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PRIOR APPLICATION NUMBER: 60/079294  
PRIOR FILING DATE: 1998-03-25  
PRIOR APPLICATION NUMBER: 60/079656  
PRIOR FILING DATE: 1998-03-26  
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PRIOR FILING DATE: 1998-03-27  
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PRIOR APPLICATION NUMBER: 60/079663  
PRIOR FILING DATE: 1998-03-27  
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PRIOR APPLICATION NUMBER: 60/079786  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/079920  
PRIOR FILING DATE: 1998-03-30  
PRIOR APPLICATION NUMBER: 60/079923  
PRIOR FILING DATE: 1998-03-30  
PRIOR APPLICATION NUMBER: 60/080105  
PRIOR FILING DATE: 1998-03-31  
PRIOR APPLICATION NUMBER: 60/080107  
PRIOR FILING DATE: 1998-03-31  
PRIOR APPLICATION NUMBER: 60/080165  
PRIOR FILING DATE: 1998-03-31  
PRIOR APPLICATION NUMBER: 60/080194  
PRIOR FILING DATE: 1998-03-31  
PRIOR APPLICATION NUMBER: 60/080327  
PRIOR FILING DATE: 1998-04-01  
PRIOR APPLICATION NUMBER: 60/080328  
PRIOR FILING DATE: 1998-04-01  
PRIOR APPLICATION NUMBER: 60/080333  
PRIOR FILING DATE: 1998-04-01  
PRIOR APPLICATION NUMBER: 60/080334  
PRIOR FILING DATE: 1998-04-01  
PRIOR APPLICATION NUMBER: 60/081070  
PRIOR FILING DATE: 1998-04-08

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model  
Run on: April 14, 2003, 09:33:49 ; Search time 828.5 seconds  
(without alignments)  
527.795 Million cell updates/sec

Title: US-09-821-734-13  
Perfect score: 27  
Sequence: 1 gtgcggcggtggtcttcttcctc 27

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

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Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
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8: em\_hic:\*  
9: gb\_estl:\*  
10: gb\_est2:\*  
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27: em\_gss\_rod:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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3	27	100.0	444	17	AQ053523	AQ053523 RPCI11-50
4	27	100.0	484	17	AQ636441	AQ636441 RPCI-11-4
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6	27	100.0	882	14	BO708386	BO708386 AGENCOURT

7	27	100.0	902	14	BO708480	BO708480 AGENCOURT
8	27	100.0	904	14	BQ893679	BQ893679 AGENCOURT
9	27	100.0	914	14	BQ712611	BQ712611 AGENCOURT
10	27	100.0	917	14	BQ711571	BQ711571 AGENCOURT
11	27	100.0	937	14	BQ894290	BQ894290 AGENCOURT
12	27	100.0	939	14	BQ712351	BQ712351 AGENCOURT
13	27	100.0	949	9	AL563971	AL563971 AL563971
14	27	100.0	998	14	BQ711650	BQ711650 AGENCOURT
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17	20.6	76.3	448	17	AZ773575	AZ773575 2M0001N06
18	20.6	76.3	489	17	AZ463400	AZ463400 1M0272007
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21	20.6	76.3	749	14	BQ572291	BQ572291 UI-M-FD0-
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24	20.6	76.3	804	12	BF531575	BF531575 602091233
25	20.2	74.8	923	17	CNS022R0	AL178533 Tetraodon
26	20.2	74.8	1101	14	BQ137346	BQ137346 NF065B12S
27	19.8	73.3	1049	12	BG026698	BG026698 602293545
28	19.6	72.6	350	14	W45099	W45099 zc20q11.r1
29	19.6	72.6	392	14	R86318	R86318 y062b09.r1
30	19.6	72.6	474	17	AQ556075	AQ556075 HS-2079.A
31	19.6	72.6	509	14	H08966	H08966 y19a05.r1
32	19.6	72.6	824	17	AG135962	AG135962 Pan trogl
33	19.6	72.6	1101	17	CNS05FDY	AL334879 Tetraodon
34	19.4	71.9	606	10	BE414920	BE414920 MML006.G0
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ALIGNMENTS

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DEFINITION AV692993 GK Homo sapiens cDNA clone GKCDDB09 5', mRNA sequence.  
ACCESSION AV692993  
VERSION AV692993.1 GI:10294856  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens

REFERENCE  
AUTHORS Xiao, H., Huang, J., Xu, Z., Qian, B., Zhu, Z., Yan, Q., Cai, T., Zhang, X.,  
Xiao, H., Qu, J., Liu, F., Huang, Q., Cheng, Z., Li, N., Du, J., Hu, W.,  
Shen, K., Lu, G., Fu, G., Zhong, M., Xu, S., Gu, W., Huang, W., Zhao, X.,  
Hu, G., Gu, J., Chen, Z. and Han, Z.  
Insight into hepatocellular carcinogenesis at transcriptome level  
by comparing gene expression profiles of hepatocellular carcinoma  
with those of corresponding noncancerous liver  
Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)  
21625106

JOURNAL  
MEDLINE  
COMMENT Contact: Zequang Han  
Chinese National Human Genome Center at Shanghai  
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai  
201203, P. R. China  
Tel: 86-21-50801919(ex.45)  
Fax: 86-21-50801922  
Email: hanzq@chgc.sh.cn  
This clone is available at CHGC in Shanghai.

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/lab_stage="Adult"
/lab_host="SOLR"
/notes="vector: pbluescript sk(-); Site_1: EcoRI; Site_2:
XhoI"
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Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGCTGGCGGGTGGCTTCTTCTCTC 27
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Db 232 GTGCTGGCGGGTGGCTTCTTCTCTC 258
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RESULT 2
AW898913
LOCUS
DEFINITION
CH0-NN0079-140400-334-f10 NN0079 Homo sapiens cDNA, mRNA sequence.
ACCESSION
AW898913
VERSION
AW898913.1 GI:8063118
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
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Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
M.J., Soares,F., Brentani,R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=et2-CM0-NN0079-140
400-334-f10&t3=2000-04-14&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 420.
Location/Qualifiers
1. 420
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="NN0079"
/dev_stage="Adult"
/notes="Organ: nervous_normal; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
BASE COUNT      118 a 100 c 89 g 113 t

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## ORIGIN

```

Query Match      100.0%; Score 27; DB 10; Length 420;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGCTGGCGGGTGGCTTCTTCTCTC 27
|||||
Db 82 GTGCTGGCGGGTGGCTTCTTCTCTC 108
|||||

RESULT 3
AQ053523
LOCUS
DEFINITION
RPC11-50L10.TJ RPC1-11 Homo sapiens genomic clone RPC1-11-50L10,
DNA sequence.
ACCESSION
AQ053523
VERSION
AQ053523.1 GI:3348446
KEYWORDS
GSS.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 444)
Adams,M.D., Rounsley,S.D., Zhao,S., Field,C.E., Bass,S., Linher,K.,
Golden,K., Berry,K., Granger,D., Suh,E., Wibie,C., de Jong,P. and
Venter,J.C.
Use of BAC End Sequences for Sequence-Ready Map Building (1998)
Unpublished (1998)
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: mdadams@tigr.org
Clones are derived from the human BAC library RPC1-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genetics (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Class: BAC ends.
Location/Qualifiers
1. 444
/organism="Homo sapiens"
/db_xref="GDB:7519089"
/db_xref="taxon:9606"
/clone="RPC1-11-50L10"
/clone_lib="RPC1-11"
/sex="Male"
/cell_type="Lymphocytes"
/notes="Vector: pBACE3.6; Site_1: EcoRI; Site_2: EcoRI;
RPC11 Human Male BAC Library"
BASE COUNT      62 a 120 c 173 g 89 t
ORIGIN
Query Match      100.0%; Score 27; DB 17; Length 444;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGCTGGCGGGTGGCTTCTTCTCTC 27
|||||
Db 204 GTGCTGGCGGGTGGCTTCTTCTCTC 230
|||||

RESULT 4
AQ636441
LOCUS
DEFINITION
RPC1-11-477N9.TJ RPC1-11 Homo sapiens genomic clone RPC1-11-477N9,
DNA sequence.
ACCESSION
AQ636441
VERSION
AQ636441.1 GI:5099076

```

## FEATURES source

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BASE COUNT      62 a 120 c 173 g 89 t
ORIGIN
Query Match      100.0%; Score 27; DB 17; Length 444;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGCTGGCGGGTGGCTTCTTCTCTC 27
|||||
Db 204 GTGCTGGCGGGTGGCTTCTTCTCTC 230
|||||

RESULT 4
AQ636441
LOCUS
DEFINITION
RPC1-11-477N9.TJ RPC1-11 Homo sapiens genomic clone RPC1-11-477N9,
DNA sequence.
ACCESSION
AQ636441
VERSION
AQ636441.1 GI:5099076

```

GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model  
Run On: April 14, 2003; 09:31:34 ; Search time 523.667 Seconds  
(without alignments)  
1500.527 Million cell updates/sec

Title: US-09-821-734-14  
Perfect score: 27  
Sequence: 1 gagtagcacattatgatgtctgttg 27

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues  
Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl.\*

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- 2: gb\_htg.\*
- 3: gb\_in.\*
- 4: gb\_om.\*
- 5: gb\_ov.\*
- 6: gb\_pat.\*
- 7: gb\_ph.\*
- 8: gb\_pl.\*
- 9: gb\_pr.\*
- 10: gb\_ro.\*
- 11: gb\_sts.\*
- 12: gb\_sy.\*
- 13: gb\_un.\*
- 14: gb\_vt.\*
- 15: em\_ba.\*
- 16: em\_fun.\*
- 17: em\_hum.\*
- 18: em\_in.\*
- 19: em\_mu.\*
- 20: em\_om.\*
- 21: em\_or.\*
- 22: em\_ov.\*
- 23: em\_pat.\*
- 24: em\_ph.\*
- 25: em\_pi.\*
- 26: em\_ro.\*
- 27: em\_sts.\*
- 28: em\_un.\*
- 29: em\_vt.\*
- 30: em\_htg\_hum.\*
- 31: em\_htg\_inv.\*
- 32: em\_htg\_other.\*
- 33: em\_htg\_mus.\*
- 34: em\_htg\_pln.\*
- 35: em\_htg\_rod.\*
- 36: em\_htg\_mam.\*
- 37: em\_htg\_vrt.\*
- 38: em\_sy.\*
- 39: em\_htgo\_hum.\*
- 40: em\_htgo\_mus.\*
- 41: em\_htgo\_other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	27	100.0	27	6	AX268376	Sequence
2	27	100.0	198	9	AF016828	Homo sapi
3	27	100.0	592	9	HA7318	Homo sapi
4	27	100.0	2253	6	AX467227	Sequence
5	27	100.0	2253	9	AY101595	Homo sapi
6	27	100.0	2472	9	BC025672	Homo sapi
7	27	100.0	2518	9	AF176574	Homo sapi
8	27	100.0	2653	6	AX337498	Sequence
9	27	100.0	2653	6	I23794	Sequence 1
10	27	100.0	2653	9	HUMPSM	Human prot
11	27	100.0	117521	2	AC023784	Homo sapi
12	27	100.0	129095	9	AC110742	Homo sapi
13	27	100.0	158524	2	AL162372	Homo sapi
14	27	100.0	187638	2	AC118273	Homo sapi
15	27	100.0	246865	2	AC074003	Homo sapi
16	25.4	94.1	2061	6	AX403107	Sequence
17	25.4	94.1	2558	6	AX376036	Sequence
18	25.4	94.1	93525	9	AF007544	Homo sapi
19	25.4	94.1	135637	9	AF003400	Homo sapi
20	25.4	94.1	192648	2	AC024234	Homo sapi
21	22.2	82.2	2532	4	AF050502	Sus scrofa
22	20.6	76.3	2259	10	AF513486	Rattus no
23	20.6	76.3	2348	10	AF040256	Rattus no
24	20.6	76.3	2899	10	RNU75973	Rattus norv
25	20.6	76.3	234784	2	AC106536	Rattus no
26	20.6	76.3	235731	2	AC097423	Rattus no
27	19.8	73.3	186191	2	AC126532	Rattus no
28	19.6	72.6	653	11	G56278	SHGC-101792
29	19.6	72.6	2314	3	AY060661	Drosophila
30	19.6	72.6	32819	2	AC014478	Drosophila
31	19.6	72.6	65558	2	AC116742	Mus muscu
32	19.6	72.6	71307	2	AC008296	Drosophila
33	19.6	72.6	82600	8	AP005149	Oryza sat
34	19.6	72.6	83684	9	AC105290	Homo sapi
35	19.6	72.6	83714	2	AC008297	Drosophila
36	19.6	72.6	103889	8	ATT24C20	Arabidops
37	19.6	72.6	146174	2	AC095369	Rattus no
38	19.6	72.6	154066	9	HS24018	Human DNA
39	19.6	72.6	154216	9	AC073071	Homo sapi
40	19.6	72.6	164682	9	AC006199	Homo sapi
41	19.6	72.6	165080	2	AC117493	Homo sapi
42	19.6	72.6	175335	3	AC091636	Drosophila
43	19.6	72.6	177607	9	AC090642	Homo sapi
44	19.6	72.6	178216	2	AC051662	Homo sapi
45	19.6	72.6	190478	2	AC130127	Rattus no

ALIGNMENTS

RESULT 1  
AX268376  
LOCUS AX268376  
DEFINITION Sequence 14 from Patent WO0174845.  
ACCESSION AX268376  
VERSION AX268376.1 GI:16541583  
KEYWORDS synthetic construct.  
SOURCE synthetic construct.  
ORGANISM artificial sequences.  
REFERENCE 1  
Pedyczak, A., Chong, P. and Sia, C. D.  
AUTHORS Immunogenic peptides derived from prostate-specific membrane  
TITLE antigen (psma) and uses thereof  
JOURNAL Patent: WO 0174845-A 14 11-OCT-2001;

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FEATURES
  source
    Adventis Pasteur Limited (CA)
    Location/Qualifiers
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        /organism="synthetic construct"
        /db_xref="taxon:32630"
        /note="CLP330"
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  ORIGIN
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    Best Local Similarity 100.0%; Pred. No. 0.038;
    Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGCTAGCACATTATGATGCTCTGTTG 27
      |||
Db 1 GAGCTAGCACATTATGATGCTCTGTTG 27

RESULT 2
AF016828 Homo sapiens prostate specific-membrane antigen gene, provisional
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
  Homo sapiens.
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
  Noack,B., Pillarsky,C.P., Schmidt,U., Froehner,M. and Wirth,M.P.
  A new splice variant of prostate-specific membrane antigen
  Unpublished
  2 (bases 1 to 592)
  Noack,B.
  Direct Submission
  Submitted (28-JUN-1998) Noack B., Department of Urology, Technical
  University of Dresden, Fetscherstr. 74, Dresden 01307, GERMANY
  Related sequence: AF007544, M99487.
  Location/Qualifiers
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      /db_xref="taxon:9606"
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      /tissue_type="prostatic carcinoma metastatic lymph node"
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    208 a 120 c 107 g 157 t

BASE COUNT      208 a 120 c 107 g 157 t
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  Query Match      100.0%; Score 27; DB 9; Length 592;
  Best Local Similarity 100.0%; Pred. No. 0.042;
  Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGCTAGCACATTATGATGCTCTGTTG 27
      |||
Db 340 GAGCTAGCACATTATGATGCTCTGTTG 366

RESULT 4
AX467227
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
  human.
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

```

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 14, 2003, 09:27:29 ; Search time 99 seconds  
(without alignments)  
614.181 Million cell updates/sec

Title: US-09-821-734-14

Perfect score: 27

Sequence: 1 gagctagcattatgatgtcctgttg 27

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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23: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.\*  
24: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	27	100.0	27	22	Human DNA encoding
2	27	100.0	60	24	Human spliced tran
3	27	100.0	866	21	Human prostate can
4	27	100.0	2226	21	DNA encoding a hum
5	27	100.0	2253	21	Human prostate spe
6	27	100.0	2653	15	Prostate-specific
7	27	100.0	2653	15	CDNA encoding huma
8	27	100.0	2653	24	Human benign prost
9	27	100.0	2653	24	prostate cancer re

10	27	100.0	2654	17	AAT36785	prostate-specific
11	27	100.0	2884	23	ABV22873	Human prostate exp
12	27	100.0	2884	23	ABV23013	Human prostate exp
13	27	100.0	2884	23	ABV28703	Human prostate exp
14	27	100.0	2884	23	ABV28849	Human prostate exp
15	25.4	94.1	2061	24	AAD34009	Human gene 4 cDNA.
16	25.4	94.1	2558	21	AAC78599	Human PRO739 nucle
17	25.4	94.1	2558	22	AAS45976	Human DNA encoding
18	22.4	83.0	789	17	AAT36779	prostate-specific
19	22.4	83.0	1280	17	AAT36789	prostate-specific
20	19.6	72.6	1077	21	AAC50963	Arabidopsis thalia
21	19.6	72.6	3527	23	ABL28852	Drosophila melanog
22	19.6	70.4	1143	21	AAC79245	Human lung tumour-
23	19.6	70.4	1143	23	AAD23321	Human lung tumour-
24	19.6	70.4	1414	23	AAS79889	DNA encoding novel
25	18.6	68.9	279	23	ABV60526	Human prostate exp
26	18.4	68.1	22	22	AAD17635	Human GCPII gene e
27	18.2	67.4	489	21	AAF11645	Aspergillus niger
28	18.6	66.7	580	22	ABA59984	Human foetal liver
29	18.6	66.7	580	22	AAK08255	Human brain expres
30	18.6	66.7	580	22	AAK34134	Human bone marrow
31	18.6	66.7	580	22	AAI39857	Probe #8543 used t
32	18.6	66.7	580	24	ABS08897	Human genome-deriv
33	18.6	66.7	2449	23	ABL21808	Drosophila melanog
34	18.6	66.7	2456	23	ABL21846	Genomic fragment #
35	18.6	66.7	48328	22	AAF28540	Arabidopsis thalia
36	17.6	65.2	1564	21	AAC33440	TCV S1 protein cod
37	17.6	65.2	2297	20	AAK4085	TCV S1 protein cod
38	17.6	65.2	2297	20	AAK4084	TCV S1 protein cod
39	17.6	65.2	2297	20	AAK4086	TCV S1 protein cod
40	17.6	65.2	2297	20	AAK4091	TCV S1 protein cod
41	17.6	65.2	3738	13	AAQ31412	Bacillus thuringie
42	17.6	65.2	3738	18	AAT66802	Bacillus thuringie
43	17.6	65.2	3738	18	AAT60045	8603a toxin coding
44	17.6	65.2	3738	19	AAV58982	B.t. toxin gene 86
45	17.6	65.2	3738	21	AAA65094	Bacillus thuringie

#### ALIGNMENTS

RESULT 1  
AAS15141 standard; DNA; 27 BP.

AC AAS15141;

DT 16-JAN-2002 (first entry)

DE Human DNA encoding a PSMA derived immunogenic peptide CLP330.

Human; ds; PSMA; prostate specific membrane antigen; prostate cancer;  
tumour; immunogenic peptide; cytostatic; gene therapy; CLP330.

OS Homo sapiens.

XX Key Location/Qualifiers

FH CDS 1..27

FT /\*tag= a.

FT /product= "CLP330"

FT /partial

FT /note= "No start or stop codon"

XX WO200174845-A2.

PN 11-OCT-2001.

XX 30-MAR-2001; 2001WO-CA00411.

XX 31-MAR-2000; 2000US-193386P.

XX (AVET ) AVENTIS PASTEUR LTD.

PI Pedyczak A, Chong P, Sia CDY;  
 DR WPI; 2001-626378/72.  
 DR P-PSDB; AAU09106.  
 XX  
 PT New polypeptides useful for inducing an immune response and treating  
 PT prostate cancer comprises polypeptides derived from the prostate  
 PT specific membrane antigen -  
 XX  
 PS Claim 6; Page 15; 47pp; English.  
 XX  
 CC The invention relates to prostate specific membrane antigen (PSMA)  
 CC derived peptides (and the nucleic acids encoding them) capable of  
 CC eliciting an immune response. The molecules of the invention are used to  
 CC elicit an immune response, particularly to treat cancer and tumours,  
 CC especially prostate cancer. Delivery of the peptides may be by  
 CC expression from the nucleic acids encoding them (i.e. gene therapy).  
 CC The present sequence encodes a PSMA derived immunogenic peptide.  
 XX  
 SQ Sequence 27 BP; 6 A; 5 C; 7 G; 9 T; 0 other;  
 Query Match 100.0%; Score 27; DB 22; Length 27;  
 Best Local Similarity 100.0%; Pred. No. 0.0012;  
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GAGCTAGCACATTATGATGTCCTGTTG 27  
 DB 1 GAGCTAGCACATTATGATGTCCTGTTG 27  
 RESULT 2  
 ABN42303  
 ID ABN42303 standard; DNA; 60 BP.  
 XX  
 AC ABN42303;  
 XX  
 DT 15-JUL-2002 (first entry)  
 XX  
 DE Human spliced transcript detection oligonucleotide SEQ ID NO:15051.  
 XX  
 KW Human; mouse; rat; splice transcript; detection; RNA transcript;  
 KW splice variant; transcriptome; oligonucleotide library; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200210449-A2.  
 XX  
 PD 07-FEB-2002.  
 XX  
 PF 20-JUL-2001; 2001WO-1801903.  
 XX  
 PR 28-JUL-2000; 2000US-221607P.  
 PR 02-MAY-2001; 2001US-287724P.  
 XX  
 PA (COMP-) COMPUGEN INC.  
 XX  
 XX Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;  
 PI WPI; 2002-257383/30.  
 XX  
 DR New oligonucleotide libraries comprising oligonucleotides which  
 PT selectively hybridize to mRNAs transcribed from a transcription unit of  
 PT a genome, useful for detecting tissue-, pathology-, and  
 PT developmental-specific genes -  
 XX  
 PS Example 1; SEQ ID 15051; 47pp; English.  
 XX  
 CC The present invention describes oligonucleotide libraries for detecting  
 CC messenger RNAs that populate a (sub-)transcriptome, where the  
 CC (sub-)transcriptome comprises messenger RNAs transcribed from multiple  
 CC transcription units that populate a genome. The library comprises  
 CC several oligonucleotides, each capable of hybridising selectively to a  
 CC set of messenger RNAs transcribed from a given transcription unit of

CC the genome, which encodes one or more messenger RNA splice variants.  
 CC The oligonucleotide libraries are useful for detecting mRNAs from a  
 CC biological sample, in expression profiling studies, in qualitatively or  
 CC quantitatively characterising the corresponding transcriptome, and in  
 CC detecting RNA transcripts and splice variants of human or animal  
 CC transcriptomes. The libraries may also be used as specialised mini  
 CC libraries to detect transcripts of a sub-transcriptome under a  
 CC particular biological or pathological state, and so allowing the  
 CC detection of tissue- and pathology-specific genes such as those genes  
 CC only expressed in specific tissue under a specific pathological  
 CC condition; to detect developmental specific genes; and to detect RNA  
 CC transcripts and splice variants of a transcriptome of a patient suffering  
 CC from a particular disorder. ABN27253 to ABN59589 represent  
 CC oligonucleotide sequences from rats, humans and mice, which are used in  
 CC the exemplification of the present invention.  
 CC N.B. The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences.  
 XX  
 SQ Sequence 60 BP; 17 A; 17 C; 9 G; 17 T; 0 other;  
 Query Match 100.0%; Score 27; DB 24; Length 60;  
 Best Local Similarity 100.0%; Pred. No. 0.0014;  
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GAGCTAGCACATTATGATGTCCTGTTG 27  
 DB 4 GAGCTAGCACATTATGATGTCCTGTTG 30  
 RESULT 3  
 AAF15696  
 ID AAF15696 standard; cDNA; 866 BP.  
 XX  
 AC AAF15696;  
 XX  
 DT 13-MAR-2001 (first entry)  
 XX  
 DE Human prostate cancer antigen nucleotide sequence SEQ ID NO:131.  
 XX  
 KW Human; prostate cancer; prostate cancer antigen; detection; diagnosis;  
 KW neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular;  
 KW vulnery; gastrointestinal; nephrotropic; antineoplastic; gynaecological;  
 KW antibacterial; gene therapy; neural; immune; reproductive; renal;  
 KW gastrointestinal; pulmonary; cardiovascular; proliferative disorder;  
 KW wound; infectious disease; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200055174-A1.  
 XX  
 PD 21-SEP-2000.  
 XX  
 PF 08-MAR-2000; 2000WO-US05988.  
 XX  
 PR 12-MAR-1999; 99US-0124270.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 PA (ROSE/) ROSEN C A.  
 XX  
 PI Rosen CA, Ruben SM;  
 XX  
 XX WPI; 2000-587513/55.  
 DR P-PSDB; AAB56493.  
 XX  
 PT Prostate cancer associated gene sequences, referred to as prostate  
 PT cancer antigens, useful for treatment, prevention, and diagnosis of  
 PT disorders such as prostate cancer -  
 XX  
 PS Claim 1; Page 697-698; 2338pp; English.  
 XX  
 CC AAF15566 to AAF16505 encode the human prostate cancer associated  
 CC proteins, called prostate cancer antigens, given in AAB56163 to AAB57302.



GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 14, 2003, 10:10:25 ; Search time 21 Seconds  
(without alignments)  
394.299 Million cell updates/sec

Title: US-09-821-734-14

Perfect score: 27

Sequence: 1 gagctagcacattatgatgctctgttg 27

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_NA:\*

- 1: /cgn2.6/ptodata/1/ina/5A\_COMB.seq:\*
- 2: /cgn2.6/ptodata/1/ina/5B\_COMB.seq:\*
- 3: /cgn2.6/ptodata/1/ina/6A\_COMB.seq:\*
- 4: /cgn2.6/ptodata/1/ina/6B\_COMB.seq:\*
- 5: /cgn2.6/ptodata/1/ina/PCTUS\_COMB.seq:\*
- 6: /cgn2.6/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	27	100.0	2133	4	US-09-164-034B-1
2	27	100.0	2653	1	US-08-325-553-1
3	27	100.0	2653	2	US-08-394-152A-1
4	22.4	83.0	789	2	US-08-394-152A-42
5	19	70.4	1143	4	US-09-370-838-287
C 6	17.6	65.2	3738	1	US-08-158-232-7
C 7	17.6	65.2	3738	1	US-08-304-626-7
C 8	17.6	65.2	3738	1	US-08-611-928-7
C 9	17.6	65.2	3738	3	US-09-173-891-7
C 10	17.4	64.4	1194	4	US-09-134-001C-1267
C 11	17.4	64.4	5519	1	US-09-453-702B-226
C 12	17	63.0	2457	1	US-08-486-013-68
C 13	17	63.0	2457	2	US-08-482-279-68
C 14	17	63.0	2457	2	US-08-342-268-68
C 15	17	63.0	2457	3	US-09-015-968-68
C 16	17	63.0	2457	4	US-09-397-386-68
C 17	17	63.0	90050	4	US-09-245-041-5
C 18	16.6	61.5	152331	3	US-09-128-155-17
C 19	16.6	61.5	176373	3	US-09-128-155-17
C 20	16.4	60.7	669	4	US-09-134-001C-216
21	16.4	60.7	1066	5	PCT-US92-00282-14
22	16.2	60.0	302	4	US-09-060-756-253
C 23	16.2	60.0	741	4	US-09-199-637A-406
C 24	16.2	60.0	3597	4	US-09-199-637A-404
25	16.2	60.0	8075	3	US-08-374-077C-1
26	16.2	60.0	8075	4	US-08-895-590-1
27	16.2	60.0	8075	4	US-09-539-879A-1

28	16.2	60.0	42235	4	US-09-199-637A-1	Sequence 1, Appli
29	16	59.3	1741	4	US-09-232-160-4	Sequence 4, Appli
30	16	59.3	1974	1	US-08-413-135-3	Sequence 3, Appli
31	16	59.3	1974	4	US-08-971-395-3	Sequence 3, Appli
32	16	59.3	3054	4	US-09-484-970B-138	Sequence 138, App
C 33	16	59.3	44453	4	US-09-146-053-5	Sequence 5, Appli
34	16	59.3	84495	4	US-09-797-906-3	Sequence 3, Appli
35	15.8	58.5	1221	3	US-08-965-600-2	Sequence 2, Appli
36	15.8	58.5	1221	4	US-09-489-506-2	Sequence 1, Appli
37	15.8	58.5	1247	2	US-08-647-960-1	Sequence 1, Appli
C 38	15.8	58.5	1952	3	US-08-714-918-39	Sequence 39, Appl
C 39	15.8	58.5	1952	4	US-09-263-315-39	Sequence 39, Appl
C 40	15.8	58.5	1952	4	US-09-263-315-39	Sequence 39, Appl
C 41	15.8	58.5	1952	4	US-09-266-417-39	Sequence 39, Appl
42	15.8	58.5	2418	3	US-08-669-286-4	Sequence 4, Appli
43	15.8	58.5	2418	4	US-09-469-253-4	Sequence 4, Appli
44	15.8	58.5	2418	4	US-09-642-146-4	Sequence 4, Appli
45	15.8	58.5	3003	4	US-09-423-340-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1

US-09-164-034B-1

GENERAL INFORMATION:

APPLICANT: Mincheff, Milcho S.

APPLICANT: Loukinov, I. Dmitri

Zoubak, Serquet

TITLE OF INVENTION: Immunotherapy of Cancer Through Expression

of Truncated Tumor- or Tumor-Associated Antigen

NUMBER OF SEQUENCES: 1

CORRESPONDENCE ADDRESS:

ADDRESSER: William S. Ramsey,

Ramsey, Cook, Looper & Kurlander, LLC

STREET: 10420 Little Patuxent Parkway, Suite 250

City: Columbia

STATE: Maryland

COUNTRY: USA

Zip: 21044

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage

COMPUTER: PC

OPERATING SYSTEM: Windows 95

SOFTWARE: WordPerfect 8

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/164,034B

FILING DATE: 30-Sep-1998

ATTORNEY/AGENT INFORMATION:

NAME: Ramsey, William S.

REGISTRATION NUMBER: 32,715

REFERENCE/DOCKET NUMBER: brll

TELECOMMUNICATION INFORMATION:

TELEPHONE: (410) 992-9660

TELEFAX: (410) 992-9540

SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-09-164-034B-1

Query Match 100.0%; Score 27; DB 4; Length 2133;  
Best Local Similarity 100.0%; Pred No. 0.00018;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGCTAGCACATTATGATGCTCTGTG 27  
|||||  
DB 199 GAGCTAGCACATTATGATGCTCTGTG 225

RESULT 2

US-08-325-553-1

Sequence 1, Application US/08325553

Patent No. 5538866

GENERAL INFORMATION:

APPLICANT: Israeli, Ron S.

APPLICANT: Heston, Warren D.W.  
APPLICANT: Fair, William R.  
TITLE OF INVENTION: THE PROSTATE-SPECIFIC MEMBRANE ANTIGEN  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cooper & Dunham  
STREET: 30 Rockefeller Plaza  
CITY: New York  
STATE: New York  
COUNTRY: United States of America  
ZIP: 10112  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/325.553  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/973.337A  
FILING DATE: 05 NOV 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 1747/41426  
TELEPHONE: (212) 977-9550  
TELEFAX: (212) 664-0525  
TELEX: 422523 COOP UI  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2653 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
TISSUE TYPE: Carcinoma  
IMMEDIATE SOURCE:  
CLONE: Prostate-Specific Membrane Antigen  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 262..2511  
US-08-325-553-1

Query Match 100.0%; Score 27; DB 1; Length 2653;  
Best Local Similarity 100.0%; Pred. No. 0.00019;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGCTAGCACATTATGATGCTCTGTG 27  
|||||  
Db 586 GAGCTAGCACATTATGATGCTCTGTG 612

## RESULT 3

US-08-394-152A-1  
Sequence 1, Application US/08394152A  
Patent No. 5935818  
GENERAL INFORMATION:  
APPLICANT: Israeli, Ron S.  
APPLICANT: Heston, Warren D.W.  
APPLICANT: Fair, William R.  
TITLE OF INVENTION: PROSTATE-SPECIFIC MEMBRANE ANTIGEN AND  
TITLE OF INVENTION: USES THEREOF  
NUMBER OF SEQUENCES: 48  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cooper & Dunham LLP  
STREET: 1185 Avenue of the Americas

CITY: New York  
STATE: New York  
COUNTRY: United States of America  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM 330 466 DX2  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/394.152A  
FILING DATE: 24-FEB-95  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 41426-B  
TELEPHONE: (212) 278-0400  
TELEFAX: (212) 391-0525  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2653 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
TISSUE TYPE: Carcinoma  
IMMEDIATE SOURCE:  
CLONE: Prostate-Specific Membrane Antigen  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 262..2511  
US-08-394-152A-1

Query Match 100.0%; Score 27; DB 2; Length 2653;  
Best Local Similarity 100.0%; Pred. No. 0.00019;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGCTAGCACATTATGATGCTCTGTG 27  
|||||  
Db 586 GAGCTAGCACATTATGATGCTCTGTG 612

## RESULT 4

US-08-394-152A-42  
Sequence 42, Application US/08394152A  
Patent No. 5935818  
GENERAL INFORMATION:  
APPLICANT: Israeli, Ron S.  
APPLICANT: Heston, Warren D.W.  
APPLICANT: Fair, William R.  
TITLE OF INVENTION: PROSTATE-SPECIFIC MEMBRANE ANTIGEN AND  
TITLE OF INVENTION: USES THEREOF  
NUMBER OF SEQUENCES: 48  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cooper & Dunham LLP  
STREET: 1185 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: United States of America  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM 330 466 DX2  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/394.152A

GenCore version 5.1.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 14, 2003, 13:13:08 ; Search time 33.6667 seconds  
(without alignments)  
703.471 Million cell updates/sec

Title: US-09-821-734-14

Perfect score: 27

Sequence: 1 gagctagcacattatgatctctgttg 27

Scoring table: IDENTITY\_NUC

Gapop 10\_0 , Gapext 1.0

Searched: 593429 segs, 438583890 residues

Total number of hits satisfying chosen parameters: 1186858

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications\_NA.\*

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3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq.\*  
4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq.\*  
5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq.\*  
6: /cgn2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq.\*  
7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq.\*  
8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq.\*  
9: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq.\*  
10: /cgn2\_6/ptodata/1/pubpna/US09\_PUBCOMB.seq.\*  
11: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq.\*  
12: /cgn2\_6/ptodata/1/pubpna/US10\_PUBCOMB.seq.\*  
13: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq.\*  
14: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq.\*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	27	100.0	27	9	US-09-821-734-14
2	27	100.0	866	10	US-09-925-300-131
3	27	100.0	2653	9	US-10-094-699-2
4	27	100.0	2653	10	US-09-969-708-536
5	25.4	94.1	2558	9	US-09-978-295A-617
6	25.4	94.1	2558	9	US-09-978-697-617
7	25.4	94.1	2558	9	US-09-978-192A-617
8	25.4	94.1	2558	9	US-09-999-832A-617
9	25.4	94.1	2558	9	US-09-978-189-617
10	25.4	94.1	2558	9	US-10-174-590-103
11	25.4	94.1	2558	9	US-10-176-758-103
12	25.4	94.1	2558	9	US-10-175-737-103
13	25.4	94.1	2558	9	US-10-175-706-103
14	25.4	94.1	2558	9	US-10-175-738-103
15	25.4	94.1	2558	9	US-10-175-752-103
16	25.4	94.1	2558	9	US-10-176-482-103
17	25.4	94.1	2558	9	US-10-176-757-103
18	25.4	94.1	2558	9	US-10-176-913-103
19	25.4	94.1	2558	9	US-10-180-552-103

20	25.4	94.1	2558	9	US-10-180-557-103	Sequence 103, App
21	25.4	94.1	2558	9	US-10-173-700-103	Sequence 103, App
22	25.4	94.1	2558	9	US-10-174-572-103	Sequence 103, App
23	25.4	94.1	2558	9	US-10-174-579-103	Sequence 103, App
24	25.4	94.1	2558	9	US-10-174-582-103	Sequence 103, App
25	25.4	94.1	2558	9	US-10-174-588-103	Sequence 103, App
26	25.4	94.1	2558	9	US-10-175-739-103	Sequence 103, App
27	25.4	94.1	2558	9	US-10-175-740-103	Sequence 103, App
28	25.4	94.1	2558	9	US-10-175-743-103	Sequence 103, App
29	25.4	94.1	2558	9	US-10-176-488-103	Sequence 103, App
30	25.4	94.1	2558	9	US-10-176-492-103	Sequence 103, App
31	25.4	94.1	2558	9	US-10-176-747-103	Sequence 103, App
32	25.4	94.1	2558	9	US-10-176-750-103	Sequence 103, App
33	25.4	94.1	2558	9	US-10-176-985-103	Sequence 103, App
34	25.4	94.1	2558	9	US-10-176-987-103	Sequence 103, App
35	25.4	94.1	2558	9	US-10-176-991-103	Sequence 103, App
36	25.4	94.1	2558	9	US-10-176-992-103	Sequence 103, App
37	25.4	94.1	2558	9	US-10-176-993-103	Sequence 103, App
38	25.4	94.1	2558	9	US-10-184-658-103	Sequence 103, App
39	25.4	94.1	2558	9	US-10-173-695-103	Sequence 103, App
40	25.4	94.1	2558	9	US-10-173-697-103	Sequence 103, App
41	25.4	94.1	2558	9	US-10-173-705-103	Sequence 103, App
42	25.4	94.1	2558	9	US-10-174-576-103	Sequence 103, App
43	25.4	94.1	2558	9	US-10-174-585-103	Sequence 103, App
44	25.4	94.1	2558	9	US-10-174-586-103	Sequence 103, App
45	25.4	94.1	2558	9	US-10-175-747-103	Sequence 103, App

## ALIGNMENTS

### RESULT 1

US-09-821-734-14

; Sequence 14, Application US/09821734

; Publication No. US20030027246A1

; GENERAL INFORMATION:

; APPLICANT: Chong, Pele

; APPLICANT: Pedyczak, Artur

; APPLICANT: Sia, Charles Dwo Yuan

; TITLE OF INVENTION: Immunogenic Peptides Derived from Prostate-Specific Membrane

; FILE OF INVENTION: (PSMA) and Uses Thereof

; FILE REFERENCE: 11014-22

; CURRENT APPLICATION NUMBER: US/09/821,734

; PRIOR FILING DATE: 2001-03-30

; PRIOR APPLICATION NUMBER: US 60/193,386

; NUMBER OF SEQ ID NOS: 24

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 14

; LENGTH: 27

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: CLP330

US-09-821-734-14

Query Match 100.0%; Score 27; DB 9; Length 27;

Best Local Similarity 100.0%; Pred. No. 0.0028;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGCTAGCACATTATGATGTCCTGTG 27

|||||

DB 1 GAGCTAGCACATTATGATGTCCTGTG 27

### RESULT 2

US-09-925-300-131

; Sequence 131, Application US/09925300

; Patent No. US20020151681A1

; GENERAL INFORMATION:

; APPLICANT: Craig Rosen,

; APPLICANT: Steve Ruben

; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

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; FILE REFERENCE: PA101
; CURRENT APPLICATION NUMBER: US/09/925,300
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05988
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1890
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 131
; LENGTH: 866
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (683)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (723)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (740)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (793)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (813)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (841)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-925-300-131
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Query Match          100.0%; Score 27; DB 10; Length 866;
Best Local Similarity 100.0%; Pred. No. 0.0047;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 GAGCTAGCACATTATGATGTCCTGTTG 27
    |||||
Db 535 GAGCTAGCACATTATGATGTCCTGTTG 561
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RESULT 3
US-10-094-699-2
; Sequence 2, Application US/10094699
; Publication No. US2003004671A1
; GENERAL INFORMATION:
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; TITLE OF INVENTION: ANTI-NEOVASCULATURE PREPARATIONS FOR
; FILE REFERENCE: CTIMM 015A
; CURRENT APPLICATION NUMBER: US/10/094,699
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US 60/274,063
; PRIOR FILING DATE: 2001-03-07
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 2653
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-094-699-2
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Query Match          100.0%; Score 27; DB 9; Length 2653;
Best Local Similarity 100.0%; Pred. No. 0.0056;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 GAGCTAGCACATTATGATGTCCTGTTG 27
    |||||
Db 586 GAGCTAGCACATTATGATGTCCTGTTG 612
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RESULT 4
US-09-969-708-536
; Sequence 536, Application US/09969708
; Patent No. US20020102532A1
; GENERAL INFORMATION:
; APPLICANT: Augustus, Meena
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: Sets
; FILE REFERENCE: 689290-70
; CURRENT APPLICATION NUMBER: US/09/969,708
; CURRENT FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: US/60/237,606
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: US/60/237,608
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: US/60/237,425
; PRIOR FILING DATE: 2000-10-03
; NUMBER OF SEQ ID NOS: 658
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 536
; LENGTH: 2653
; TYPE: DNA
; ORGANISM: Homosapiens
US-09-969-708-536
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Query Match          100.0%; Score 27; DB 10; Length 2653;
Best Local Similarity 100.0%; Pred. No. 0.0056;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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    |||||
Db 586 GAGCTAGCACATTATGATGTCCTGTTG 612
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RESULT 5
US-09-978-295A-617
; Sequence 617, Application US/09978295A
; Patent No. US20020156006A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Geritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C11
; CURRENT APPLICATION NUMBER: US/09/978,295A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
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GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: April 14, 2003, 09:33:49 ; Search time 828.5 seconds  
(without alignments)  
527.795 Million cell updates/sec

Title: US-09-821-734-14

Perfect score: 27  
Sequence: 1 gagctagcattatgatgtcctgttg 27

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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1: em\_estba:\*

2: em\_esthum:\*

3: em\_estin:\*

4: em\_estmu:\*

5: em\_estov:\*

6: em\_estpl:\*

7: em\_estro:\*

8: em\_htc:\*

9: gb\_est1:\*

10: gb\_est2:\*

11: gb\_htc:\*

12: gb\_est3:\*

13: gb\_est4:\*

14: gb\_est5:\*

15: em\_estfun:\*

16: em\_estom:\*

17: gb\_gss:\*

18: em\_gss\_hum:\*

19: em\_gss\_inv:\*

20: em\_gss\_pin:\*

21: em\_gss\_vrt:\*

22: em\_gss\_fun:\*

23: em\_gss\_mam:\*

24: em\_gss\_mus:\*

25: em\_gss\_othr:\*

26: em\_gss\_pro:\*

27: em\_gss\_rod:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	27	100.0	420	10	AW898913 CM0-NN007
2	27	100.0	495	10	AW473087 xp68c02.x
3	27	100.0	704	13	BI772735 603053273
4	27	100.0	785	9	AI525231 pt1.1-2.C
5	27	100.0	809	9	AI525228 pt1.1-2.C
6	27	100.0	949	9	AL563971 AL563971

C	7	25.4	94.1	529	12	BF475484
	8	25.4	94.1	882	14	BQ708386
	9	25.4	94.1	902	14	BQ708480
	10	25.4	94.1	904	14	BQ893679
	11	25.4	94.1	909	14	BQ948549
	12	25.4	94.1	914	14	BQ712611
	13	25.4	94.1	917	14	BQ711571
	14	25.4	94.1	937	14	BQ894290
	15	25.4	94.1	938	14	BQ712351
	16	25.4	94.1	998	14	BQ711650
	17	25.4	94.1	1187	14	BM926125
	18	19.8	73.3	578	17	AQ256048
	19	19.6	72.6	303	10	BB447160
	20	19.6	72.6	415	13	BI621738
	21	19.6	72.6	415	13	BI622365
	22	19.6	72.6	468	9	AI957386
	23	19.6	72.6	653	17	AQ320303
	24	19.6	72.6	769	10	AW019789
	25	19.7	70.4	333	13	BM385103
	26	19.7	70.4	411	10	BE210798
	27	19.7	70.4	502	17	AQ623423
	28	19.7	70.4	609	17	DR5C23T
	29	19.7	70.4	657	10	BE329924
	30	19.7	70.4	710	13	BJ166802
	31	19.7	70.4	968	17	CMS06XVK
	32	19.7	70.4	996	12	BG339671
	33	18.6	68.9	371	10	BB792813
	34	18.6	68.9	549	14	BQ081352
	35	18.6	68.9	619	13	B1434493
	36	18.6	68.9	708	12	BG125123
	37	18.6	68.9	752	17	AG029187
	38	18.6	68.9	782	12	BG351593
	39	18.6	68.9	1776	17	AG079557
	40	18.2	67.4	156	17	AZ459269
	41	18.2	67.4	208	14	BQ196926
	42	18.2	67.4	385	17	AQ096129
	43	18.2	67.4	444	12	BG240159
	44	18.2	67.4	542	17	AQ393668
	45	18.2	67.4	643	12	BF796866

#### ALIGNMENTS

RESULT 1	AW898913	CM0-NN0079-140400-334-f10	NN0079	Homo sapiens	cdna	linear	EST 24-MAY-2000
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DEFINITION	AW898913	CM0-NN0079-140400-334-f10	NN0079	Homo sapiens	cdna	linear	EST 24-MAY-2000
ACCESSION	AW898913	CM0-NN0079-140400-334-f10	NN0079	Homo sapiens	cdna	linear	EST 24-MAY-2000
VERSION	AW898913.1	GI:8063118					
KEYWORDS	EST.						
SOURCE	human.						
ORGANISM	Homo sapiens						
REFERENCE	Fukuyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.						
AUTHORS	1 (bases 1 to 420)						
	Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.						
TITLE	Shotgun sequencing of the human transcriptome with ORF expressed sequence tags						
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)						
MEDLINE	20202663						
COMMENT	Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil Tel: +55-11-2704922 Fax: +55-11-2707001						

Email: asimpson@ludwig.org.br  
 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL  
 (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=st2-cm0-NN0079-140  
 400-334-fl0st3-2000-04-14st4=1)  
 Seq primer: puc 18 forward  
 High quality sequence stop: 420.

#### FEATURES

Location/Qualifiers  
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 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone\_lib="NN0079"  
 /dev\_stage="Adult"

/note="Organ: nervous\_normal; Vector: puc18; Site1: Sma1; Site2: Sma1; A mini-library was made by cloning products derived from ORSTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

118 a 100 c 89 g 113 t

#### BASE COUNT

ORIGIN

Query Match 100.0%; Score 27; DB 10; Length 420;

Best Local Similarity 100.0%; Pred. No. 0.21; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGCTAGCACATTATGATGCTCTGTTG 27

|||||

Db 328 GAGCTAGCACATTATGATGCTCTGTTG 354

#### RESULT 2

##### AW473087/c

##### LOCUS

DEFINITION AW473087 495 bp mRNA linear EST 24-FEB-2000  
 xp68c02.x2 NCI\_CGAP\_Ov39 Homo sapiens cDNA clone IMAGE:2745506 3'  
 similar to gb:M99487 PROSTATE-SPECIFIC MEMBRANE ANTIGEN (HUMAN);,  
 mRNA sequence.

##### ACCESSION

AW473087.1 GI:7043193

##### KEYWORDS

EST.

##### SOURCE

human.

##### ORGANISM

Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

##### REFERENCE

1 (bases 1 to 495)

##### AUTHORS

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

##### TITLE

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index

##### JOURNAL

Unpublished (1997)

##### COMMENT

Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-r@mail.nih.gov  
 Tissue Procurement: Andrew Berchuck M.D., John Gillespie M.D.,  
 Michael R. Emmert-Buck, M.D., Ph.D.  
 cDNA Library Preparation: David B. Krizman, Ph.D.  
 cDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 www.bio.llnl.gov/bbrp/image/image.html

Possible reversed clone: polyt not found

Seq primer: -40UP from Gibco

High quality sequence stop: 385.

#### FEATURES

Location/Qualifiers  
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 /organism="Homo sapiens"  
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 /clone="IMAGE:2745506"  
 /clone\_lib="NCI\_CGAP\_Ov39"  
 /sex="female"  
 /tissue\_type="papillary serous ovarian metastasis"  
 /lab\_host="DH10B"

/note="Organ: ovary; Vector: pAMP10; cDNA made by oligo-dT  
 priming. Non-directionally cloned into the UDG sites of  
 pAMP10. Size-selected on agarose gel, average insert  
 size 500 bp. Primary library; non-amplified. cDNA  
 Library Preparation: David B. Krizman, Ph.D (NCI).  
 Reference: Krizman et al. (1996) Cancer Research  
 56:5380-5383."

BASE COUNT 144 a 85 c 110 g 156 t

#### ORIGIN

Query Match 100.0%; Score 27; DB 10; Length 495;

Best Local Similarity 100.0%; Pred. No. 0.23; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGCTAGCACATTATGATGCTCTGTTG 27

|||||

Db 269 GAGCTAGCACATTATGATGCTCTGTTG 243

#### RESULT 3

##### BI772735

##### LOCUS

DEFINITION 603053273f1 NIH\_MGC\_122 Homo sapiens cDNA clone IMAGE:5202715,  
 mRNA sequence.

##### ACCESSION

BI772735.1 GI:15764313

##### KEYWORDS

EST.

##### SOURCE

human.

##### ORGANISM

Homo sapiens

##### REFERENCE

1 (bases 1 to 704)

##### AUTHORS

NIH-MGC http://mgc.nci.nih.gov/.

##### TITLE

National Institutes of Health, Mammalian Gene Collection (MGC)

##### JOURNAL

Unpublished (1999)

##### COMMENT

Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-r@mail.nih.gov  
 Tissue Procurement: Life Technologies, Inc.  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov

Plate: LLAM1508 row: a column: 20

High quality sequence start: 5

High quality sequence stop: 703.

#### FEATURES

Location/Qualifiers

1..704

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="IMAGE:5202715"

/clone\_lib="NIH\_MGC\_122"

/lab\_host="DH10B"

/note="Organ: pooled lung and spleen; Vector: pCMV-SPORT6;  
 Site1: NotI; Site2: EcoRV (destroyed); RNA source  
 anonymous pool of 24 week female lung, 16 week female  
 spleen, and 20-22 week male spleens. Library is oligo-dT  
 primed and directionally cloned (EcoRV site is destroyed  
 upon cloning). Average insert size 1.4 kb, insert size  
 range 1-3 kb. Library is normalized and enriched for  
 full-length clones and was constructed by C. Gruber  
 (Invitrogen). Research Genetics tracking code 026. Note:  
 this is a NIH\_MGC Library."

184 a 168 c 174 g 178 t

#### BASE COUNT

#### ORIGIN

Query Match 100.0%; Score 27; DB 13; Length 704;

Best Local Similarity 100.0%; Pred. No. 0.28; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGCTAGCACATTATGATGCTCTGTTG 27

|||||

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

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(without alignments)  
1500.527 Million cell updates/sec

Title: US-09-821-734-15  
Perfect score: 27  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: gb\_hg.\*  
3: gb\_in.\*  
4: gb\_om.\*  
5: gb\_ov.\*  
6: gb\_pat.\*  
7: gb\_ph.\*  
8: gb\_pl.\*  
9: gb\_pr.\*  
10: gb\_ro.\*  
11: gb\_sts.\*  
12: gb\_sy.\*  
13: gb\_un.\*  
14: gb\_vi.\*  
15: em\_ba.\*  
16: em\_fun.\*  
17: em\_hum.\*  
18: em\_in.\*  
19: em\_mu.\*  
20: em\_om.\*  
21: em\_of.\*  
22: em\_ov.\*  
23: em\_pat.\*  
24: em\_ph.\*  
25: em\_pl.\*  
26: em\_ro.\*  
27: em\_sts.\*  
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29: em\_vi.\*  
30: em\_htg\_hum.\*  
31: em\_htg\_inv.\*  
32: em\_htg\_other.\*  
33: em\_htg\_mus.\*  
34: em\_htg\_pln.\*  
35: em\_htg\_rod.\*  
36: em\_htg\_mam.\*  
37: em\_htg\_vit.\*  
38: em\_sy.\*  
39: em\_htgo\_hum.\*  
40: em\_htgo\_mus.\*  
41: em\_htgo\_other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	27	100.0	27	6	AX268377 Sequence
2	27	100.0	2253	6	AX467227 Sequence
3	27	100.0	2253	9	AX101595 Homo sapi
4	27	100.0	2472	9	BC025672 Homo sapi
5	27	100.0	2518	9	AF176574 Homo sapi
6	27	100.0	2558	6	AX376036 Sequence
7	27	100.0	2653	6	AX337498 Sequence
8	27	100.0	2653	6	I23794 Sequence 1
9	27	100.0	2653	9	HUMPSM
10	27	100.0	93525	9	AF007544 Homo sapi
11	27	100.0	156255	2	AF002369 Homo sapi
12	27	100.0	157527	9	AC117746 Homo sapi
13	27	100.0	158524	2	AL162372 Homo sapi
14	27	100.0	187638	2	AC118273 Homo sapi
15	27	100.0	246865	2	AC074003 Homo sapi
16	25.4	94.1	1992	9	AF261715 Homo sapi
17	25.4	94.1	2061	6	AX403107 Sequence
18	25.4	94.1	137888	9	AF003122 Homo sapi
19	25.4	94.1	192648	2	AC024234 Homo sapi
20	22.2	82.2	1428	10	AF039707 Rattus no
21	22.2	82.2	2259	10	AF513486 Rattus no
22	22.2	82.2	2348	10	AF040256 Rattus no
23	22.2	82.2	2532	4	AF050502 Sus scrof
24	22.2	82.2	2603	10	AF026380 Mus muscu
25	22.2	82.2	2899	10	U75973 Rattus norv
26	22.2	82.2	221969	2	AC106532 Rattus no
27	22.2	82.2	235731	2	AC097423 Rattus no
28	20.2	74.8	137922	2	AC073398 Homo sapi
29	20.2	74.8	155533	9	AC079177 Homo sapi
30	19.8	73.3	96460	9	HS633020 Human DNA
31	19.6	72.6	12384	1	AE012003 Xanthomon
32	19.6	72.6	61411	2	AC108846 Homo sapi
33	19.6	72.6	99183	9	AL360091 Human DNA
34	19.6	72.6	162704	2	AC016289 Homo sapi
35	19.6	72.6	187693	2	AP001502 Homo sapi
36	19.6	72.6	199347	2	AL805952 Mus muscu
37	19.6	72.6	205237	2	AL807399 Mus muscu
38	19.6	72.6	208160	2	AC124254 Homo sapi
39	19.6	72.6	212553	2	AC099581 Mus muscu
40	19.4	71.9	2004	1	ASU09240 Anabaena sp
41	19.4	71.9	2004	1	S76266 fraC=FraC I
42	19.4	71.9	341880	1	AF003589 Nostoc sp
43	19.2	71.1	468	1	AF190908 Xanthomon
44	19.2	71.1	150017	2	AL773509 Mus muscu
45	19.2	71.1	150017	2	AL844603 Mus muscu

ALIGNMENTS

RESULT 1	AX268377	Sequence 15 from Patent WO01/4845.	27 bp	DNA	linear	PAT 29-OCT-2001
LOCUS	AX268377	Sequence 15 from Patent WO01/4845.				
DEFINITION	AX268377					
ACCESSION	AX268377					
VERSION	AX268377.1	GI:16541584				
KEYWORDS		synthetic construct.				
SOURCE		synthetic construct.				
ORGANISM		artificial sequences.				
REFERENCE	1	Pedyczak A., Chong P. and Sia C.D.				
AUTHORS		Immunogenic peptides derived from prostate-specific membrane				
TITLE		antigen (psma) and uses thereof				
JOURNAL		Patent: WO 01/4845-A 15 11-OCT-2001;				

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  /db_xref="taxon:32630"
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BASE COUNT          8 a 7 c 5 g 7 t
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Query Match          100.0%; Score 27; DB 6; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.0029;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGATGTACAGCTTGGTACACACCTA 27
|||||
Db 1 CTGATGTACAGCTTGGTACACACCTA 27

RESULT 2
LOCUS               AX467227               2253 bp          DNA          linear          PAT 16-JUL-2002
DEFINITION          Sequence 1 from Patent W00234287.
ACCESSION            AX467227
VERSION              AX467227.1 GI:21900509
KEYWORDS
SOURCE              human.
ORGANISM            Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
Beier A.M., Gautam A. and Mouritsen S.R.
Novel therapeutic vaccine formulations
Patent: WO 0234287-A 1 02-MAY-2002;
Pharmexa A/S (DK)
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  /db_xref="GI:21900510"
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FSAFQCGMEGLVIVYNTARTEDFFKLERDMKINGSGKIVARIYKGVFRGNKVKNAQ
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GNFTQKVMKHIHSTNEVTRIYVICTLGAVEPDYVILGHRDWSRLQERGVAYI
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YVSFSLFSAVKNFTFETASKFSERLQDFKSNPIVLRMNDQLMFLERAFIDPLGLP
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  58..2253
  /notes="Human PSM"
BASE COUNT          670 a 448 c 527 g 608 t
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Query Match          100.0%; Score 27; DB 6; Length 2253;
Best Local Similarity 100.0%; Pred. No. 0.0055;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGATGTACAGCTTGGTACACACCTA 27
|||||
Db 1405 CTGATGTACAGCTTGGTACACACCTA 1431

RESULT 3
LOCUS               AY101595               2253 bp          mRNA          linear          PRI 27-MAY-2002
DEFINITION          Homo sapiens prostate-specific membrane antigen mRNA, complete cds.
ACCESSION            AY101595
VERSION              AY101595.1 GI:21217742
KEYWORDS
SOURCE              Homo sapiens.
ORGANISM            Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2253)
Ye, C.Z., Zhang, F.L., Zhang, Y.K. and Chen, C.Q.
Cloning and sequencing of Chinese prostate-specific membrane
antigen
Mianxue Zazhi 17 (5), 328-330 (2001)
2 (bases 1 to 2253)
Ye, C.Z.
Direct Submission
Submitted (06-MAY-2002) Department of Urology, Zhongshan Hospital,
Medical Center of Fudan University, Fenglin Rd 180, Shanghai
200032, China
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SSNEATNTPKHNKMAFLDELKAEIKKLYNTQIPLHAGTEQNOLAKIQSQNKE
FGLDSVELAHYDVLISYPNKTNPYISIIEDNGEINFNTSLFPPPGYENVSIVPPP
FSAFQCGMEGLVIVYNTARTEDFFKLERDMKINGSGKIVARIYKGVFRGNKVKNAQ
LAGAKGVILYSDPADYFAPGVKSYDPGWNLPGGVGQVGRNLLNAGDPLTPGYPANE
YAYRRTAEAVGLPSIPVHPIGYIDAKLLEKMGSGAPPDSSWRGSLKVPYNVGPGFT
GNFTQKVMKHIHSTNEVTRIYVICTLGAVEPDYVILGHRDWSRLQERGVAYI
AVVHEIVRSFGTLKKEGWRPRTILFASWDAEFGLLGSTEWAEENSRLLQERGVAYI
NADSSIEGNTLKVDCPTPLMYSLVHNLTKELSPDEGFGKSLYESWTKKSPSPFSG
MPRIKSLGSGNDFEVFORLGASGRATYKNETNKFSGYPLIHSVYETVELVERFY
DPMFKYHLTVAVQVRGGMVELANSIVLPEDCRDIYAVLRKYADKIYSISMKHPQENKT
YVSFSLFSAVKNFTFETASKFSERLQDFKSNPIVLRMNDQLMFLERAFIDPLGLP
DRPFYRHVIYAPSSHKNKYAGESFPGIYDALFDIESKVDPSKANGVEVKROIYVAATVQ
AAAEITLSEVA"
  670 a 449 c 527 g 607 t
BASE COUNT          670 a 449 c 527 g 607 t
ORIGIN

Query Match          100.0%; Score 27; DB 9; Length 2253;
Best Local Similarity 100.0%; Pred. No. 0.0055;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGATGTACAGCTTGGTACACACCTA 27
|||||
Db 1405 CTGATGTACAGCTTGGTACACACCTA 1431

RESULT 4
LOCUS               BC025672               2472 bp          mRNA          linear          PRI 11-MAR-2002
DEFINITION          Homo sapiens, Similar to folate hydrolase (prostate-specific
membrane antigen) 1, clone MGC:34488 IMAGE:5202715, mRNA, complete
cds.
ACCESSION            BC025672
VERSION              BC025672.1 GI:19343603
KEYWORDS             MGC.
SOURCE              Homo sapiens.
ORGANISM            Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```



GenCore version 5.1.3  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 14, 2003, 09:27:29 ; Search time 99 Seconds  
(without alignments)  
614.181 Million cell updates/sec

Title: US-09-821-734-15

Perfect score: 27

Sequence: 1 ctgatgtacagctgtgtacacaacct 27

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N\_Geneseq\_101002:\*

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2: /SID22/gcgdata/geneseq/geneseq-emb1/NA1981.DAT:\*  
3: /SID22/gcgdata/geneseq/geneseq-emb1/NA1982.DAT:\*  
4: /SID22/gcgdata/geneseq/geneseq-emb1/NA1983.DAT:\*  
5: /SID22/gcgdata/geneseq/geneseq-emb1/NA1984.DAT:\*  
6: /SID22/gcgdata/geneseq/geneseq-emb1/NA1985.DAT:\*  
7: /SID22/gcgdata/geneseq/geneseq-emb1/NA1986.DAT:\*  
8: /SID22/gcgdata/geneseq/geneseq-emb1/NA1987.DAT:\*  
9: /SID22/gcgdata/geneseq/geneseq-emb1/NA1988.DAT:\*  
10: /SID22/gcgdata/geneseq/geneseq-emb1/NA1989.DAT:\*  
11: /SID22/gcgdata/geneseq/geneseq-emb1/NA1990.DAT:\*  
12: /SID22/gcgdata/geneseq/geneseq-emb1/NA1991.DAT:\*  
13: /SID22/gcgdata/geneseq/geneseq-emb1/NA1992.DAT:\*  
14: /SID22/gcgdata/geneseq/geneseq-emb1/NA1993.DAT:\*  
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16: /SID22/gcgdata/geneseq/geneseq-emb1/NA1995.DAT:\*  
17: /SID22/gcgdata/geneseq/geneseq-emb1/NA1996.DAT:\*  
18: /SID22/gcgdata/geneseq/geneseq-emb1/NA1997.DAT:\*  
19: /SID22/gcgdata/geneseq/geneseq-emb1/NA1998.DAT:\*  
20: /SID22/gcgdata/geneseq/geneseq-emb1/NA1999.DAT:\*  
21: /SID22/gcgdata/geneseq/geneseq-emb1/NA2000.DAT:\*  
22: /SID22/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT:\*  
23: /SID22/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT:\*  
24: /SID22/gcgdata/geneseq/geneseq-emb1/NA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	27	100.0	27	22	AAS15142 Human DNA encoding
2	27	100.0	1037	21	AAF15651 Human prostate can
3	27	100.0	2226	21	AAA12732 Human encoding a hum
4	27	100.0	2253	21	AAA09454 Human prostate spe
5	27	100.0	2558	21	AAC78599 Human PRO739 nucle
6	27	100.0	2558	22	AAS45976 Human DNA encoding
7	27	100.0	2653	15	AAQ65520 Prostate-specific
8	27	100.0	2653	14	ABK86204 cDNA encoding huma
9	27	100.0	2653	24	ABK64556 Human benign prost

10	27	100.0	2653	24	ABL69670	Prostate cancer re
11	27	100.0	2654	17	AAT36785	Prostate-specific
12	27	100.0	2884	23	ABV22873	Human prostate exp
13	27	100.0	2884	23	ABV23013	Human prostate exp
14	27	100.0	2884	23	ABV28703	Human prostate exp
15	27	100.0	2884	23	ABV28849	Human prostate exp
16	25.4	94.1	37	22	AAI17672	PCR primer #1 used
17	25.4	94.1	1992	21	AAC61762	cDNA encoding a pr
18	25.4	94.1	2061	24	RAA34009	Human gene 4 cDNA
19	25	92.6	656	21	AAF15621	Human prostate can
20	22.2	82.2	2082	21	AAA09459	Murine prostate sp
21	22.2	82.2	2256	21	AAA09458	Murine prostate sp
22	20.8	77.0	36	22	AAI17673	PCR primer #2 used
23	19.8	73.3	1843	21	AAA61051	Maize embryo speci
24	19.8	73.3	6694	21	AAA61053	Maize embryo speci
25	18.6	68.9	128139	24	AAI64291	RVV genome nucleot
26	18.6	68.9	133719	21	AAC64754	Macaca mulatta rha
27	18	66.7	1356	20	AAI20570	Polynucleotide seq
28	18	66.7	1359	24	ABL01520	Murine apoptosis r
29	18	66.7	5752	22	AAF85087	Nucleotide sequenc
30	17.8	65.9	275	16	AAT24115	Human gene signatu
31	17.8	65.9	1006	21	AAC77762	Human cancer assoc
32	17.8	65.9	4362	22	AAI05795	Human reproductive
33	17.8	65.9	4362	23	ABK72136	Human ovarian anti
34	17.8	65.9	4362	23	ABL98359	Human testicular a
35	17.8	65.9	4362	24	ABK91728	Novel ovarian rela
36	17.6	65.2	363	21	AAC17262	Human secreted pro
37	17.6	65.2	363	21	AAZ42437	Human 5' EST isola
38	17.6	65.2	566	24	ABN64973	Human cancer relat
39	17.6	65.2	599	24	ABN64935	Human cancer relat
40	17.6	65.2	2314	22	AAI21301	Human cDNA sequenc
41	17.6	65.2	2930	22	AAF72750	Human prostate can
42	17.6	65.2	4740	22	AAI57867	Human polynucleoti
43	17.4	64.4	400	24	ABN94600	Gene #1098 used to
44	17.4	64.4	421	22	ABA56490	Human foetal liver
45	17.4	64.4	421	22	ABA65068	Human foetal liver

#### ALIGNMENTS

RESULT 1  
AAS15142  
ID AAS15142 standard; DNA; 27 BP.

XX AC AAS15142;

XX DT 16-JAN-2002 (first entry)

XX DE Human DNA encoding a PSMA derived immunogenic peptide CLP333.

XX KW Human; ds; PSMA; prostate specific membrane antigen; prostate cancer;  
XX KW tumour; immunogenic peptide; cytostatic; gene therapy; CLP333.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT CDS 1..27

FT FT /\*tag= a

FT FT /product= "CLP333"

FT FT /partial

FT FT /note= "No start or stop codon"

XX PN WO200174845-A2.

XX PD 11-OCT-2001.

XX PF 30-MAR-2001; 2001WO-CA00411.

XX PR 31-MAR-2000; 2000US-193386P.

XX PA (AVET ) AVENTIS PASTEUR LTD.

XX

```

PI Pedyczak A, Chong P, Sia CDY;
DR WPI; 2001-626378/72.
DR P-PSDB; AAU09107.
XX
XX New polypeptides useful for inducing an immune response and treating
PT prostate cancer comprises polypeptides derived from the prostate
PT specific membrane antigen -
XX
XX Claim 6; Page 15; 47pp; English.
XX
XX The invention relates to prostate specific membrane antigen (PSMA)
CC derived peptides (and the nuclei acids encoding them) capable of
CC eliciting an immune response. The molecules of the invention are used to
CC elicit an immune response, particularly to treat cancer and tumours,
CC especially prostate cancer. Delivery of the peptides may be by
CC expression from the nucleic acids encoding them (i.e. gene therapy).
CC The present sequence encodes a PSMA derived immunogenic peptide.
XX
XX Sequence 27 BP; 8 A; 7 C; 5 G; 7 T; 0 other;
SQ
Query Match 100.0%; Score 27; DB 22; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.0013;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGATGTACAGCTTGGTACACACCTA 27
    |||||
Db 1 CTGATGTACAGCTTGGTACACACCTA 27

RESULT 2
AAF15651
ID AAF15651 standard; cDNA; 1037 BP.
XX
XX AAF15651;
AC
XX
XX 13-MAR-2001 (first entry)
DT
XX
XX Human prostate cancer antigen nucleotide sequence SEQ ID NO:86.
DE
XX
XX Human; prostate cancer; prostate cancer antigen; detection; diagnosis;
KW neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular;
KW vulnery; gastrointestinal; nephrotropic; antiinfective; gynaecological;
KW antibacterial; gene therapy; neutral; immune; reproductive; renal;
KW gastrointestinal; pulmonary; cardiovascular; proliferative disorder;
KW wound; infectious disease; ss.
XX
XX Homo sapiens.
OS
XX
XX WO200055174-Al.
PN
XX
XX 21-SEP-2000.
PD
XX
XX 08-MAR-2000; 2000WO-US05988.
PF
XX
XX 12-MAR-1999; 99US-0124270.
PR
XX
XX (HUMA-) HUMAN GENOME SCI INC.
PA
XX (ROSE/) ROSEN C A.
PA
XX
XX Rosen CA, Ruben SM;
PI
XX
XX WPI; 2000-587513/55.
DR
XX P-PSDB; AAB58448.
DR
XX
XX Prostate cancer associated gene sequences, referred to as prostate
PT cancer antigens, useful for treatment, prevention, and diagnosis of
PT disorders such as prostate cancer -
XX
XX Claim 1; Page 672-673; 2338pp; English.
PS
XX
XX AAF15566 to AAF16505 encode the human prostate cancer associated
CC proteins, called prostate cancer antigens, given in AAB56363 to AAB57302.
CC

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```

CC The prostate cancer antigens can have neuroprotective, cytostatic,
CC cardioactive, immunomodulatory, muscular, vulnery, gastrointestinal,
CC nephrotropic, antiinfective, gynaecological and antibacterial activities,
CC and can be used in gene therapy. The prostate cancer antigen
CC polynucleotides may be used for detection of prostate cancer, chromosome
CC identification, as chromosome markers, and for numerous other diagnostic
CC or research purposes. The prostate cancer antigens may be used to treat
CC disorders such as neural, immune, muscular, reproductive,
CC gastrointestinal, pulmonary, cardiovascular, renal, and proliferative
CC disorders, wounds, and infectious diseases. AAF16506 to AAF16514 to
CC AAB57303 represent sequences used in the exemplification of the present
CC invention.
XX
XX Sequence 1037 BP; 337 A; 174 C; 228 G; 297 T; 1 other;
SQ
Query Match 100.0%; Score 27; DB 21; Length 1037;
Best Local Similarity 100.0%; Pred. No. 0.0031;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGATGTACAGCTTGGTACACACCTA 27
    |||||
Db 53 CTGATGTACAGCTTGGTACACACCTA 79

RESULT 3
AAF12732
ID AAF12732 standard; DNA; 2226 BP.
XX
XX AAF12732;
AC
XX
XX 25-JUL-2000 (first entry)
DT
XX
XX DNA encoding a human prostate specific membrane antigen.
DE
XX
XX Human; prostate specific membrane antigen; inactive antigen; cancer;
KW prostate cancer; ds.
KW
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH 1..2226
CDS /*tag= a
FT /product= "prostate specific membrane antigen"
FT
XX
XX WO200018933-Al.
PN
XX
XX 06-APR-2000.
PD
XX
XX 09-SEP-1999; 99WO-US20508.
PF
XX
XX 30-SEP-1998; 98US-0164034.
PR
XX
XX (AMBI-) AMERICAN FOUND BIOLOGICAL RES INC.
PA
XX (MINC/) MINCHEFF M S.
PA (LOUK/) LOUKINOV D I.
PA (ZOUB/) ZOUBAK S.
XX
XX Mincheff MS, Loukinov DI, Zoubak S;
PI
XX
XX WPI; 2000-293166/25.
DR
XX P-PSDB; AAY84667.
DR
XX
XX New DNA constructs expressing functionally inactive, altered antigens
PT are used for treating prostate cancer -
PT
XX
XX Claim 8; Page 16-18; 23pp; English.
PS
XX
XX The present sequence encodes a human prostate specific membrane
CC antigen. The polynucleotide is used to construct the DNA constructs of
CC the invention. The specification describes DNA constructs which cause
CC expression of functionally inactive, altered antigens which are
CC unaltered with respect to the efficiency of transcription and
CC translation of DNA, translation of RNA or the generation of antigen
CC

```

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 14, 2003, 10:10:25 ; Search time 21 Seconds  
(without alignments)  
394.299 Million cell updates/sec

Title: US-09-821-734-15

Perfect score: 27

Sequence: 1 ctgatgtacagcttggtacacacctta 27

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_NA:\*

- 1: /cgn2.6/ptodata/1/ina/5A\_COMB.seq:\*
- 2: /cgn2.6/ptodata/1/ina/5B\_COMB.seq:\*
- 3: /cgn2.6/ptodata/1/ina/6A\_COMB.seq:\*
- 4: /cgn2.6/ptodata/1/ina/6B\_COMB.seq:\*
- 5: /cgn2.6/ptodata/1/ina/PCTUS\_COMB.seq:\*
- 6: /cgn2.6/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	27	100.0	2133	4	US-09-164-034B-1
2	27	100.0	2653	1	US-08-325-553-1
3	27	100.0	2653	2	US-08-394-152A-1
4	17.2	63.7	5769	1	US-08-652-971-1
5	17.2	63.7	5769	2	US-08-991-258A-1
6	17.2	63.7	5769	2	US-08-769-399-1
7	17.2	63.7	5769	3	US-08-991-953A-1
8	17.2	63.7	112132	4	US-09-741-150-3
9	16.6	61.5	1952	2	US-08-481-337A-7
10	16.6	61.5	1952	4	US-09-382-256-17
11	16.6	61.5	1952	4	US-09-395-115-17
12	16.6	61.5	1952	4	US-08-436-265-17
13	16.6	61.5	1952	4	US-09-679-187-17
14	16.6	61.5	1952	5	PCT-US95-05467-7
15	16.6	61.5	2056	4	US-08-158-735A-1
16	16.6	61.5	2070	4	US-09-382-256-13
17	16.6	61.5	2070	4	US-09-395-115-13
18	16.6	61.5	2070	4	US-08-436-265-13
19	16.6	61.5	2070	4	US-09-679-187-13
20	16.6	61.5	2076	4	US-08-123-934A-3
21	16.6	61.5	2076	5	PCT-US94-10080-3
22	16.6	61.5	2252	4	US-08-462-467B-13
23	16.6	61.5	2252	4	US-08-334-179A-13
24	16.6	61.5	2402	4	US-08-462-467B-11
25	16.6	61.5	2402	4	US-08-158-735A-3
26	16.6	61.5	2402	4	US-08-334-179A-11
27	16.4	60.7	330	2	US-08-437-013-4

28	16.4	60.7	641	2	US-08-437-013-1	Sequence 1, Appli
29	16.4	60.7	641	2	US-08-437-013-28	Sequence 28, Appl
30	16.4	60.7	709	2	US-08-437-013-26	Sequence 26, Appl
31	16.4	60.7	1965	4	US-09-227-717-1	Sequence 1, Appli
32	16.4	60.7	5014	4	US-09-381-862-3	Sequence 3, Appli
33	16.4	60.7	4403765	4	US-09-103-840A-2	Sequence 2, Appli
34	16.4	60.7	4411529	4	US-09-103-840A-1	Sequence 3, Appli
35	16.2	60.0	4203	2	US-08-288-630-3	Sequence 7, Appli
36	16	59.3	536	4	US-09-347-819-7	Sequence 470, App
37	16	59.3	1001	4	US-09-641-638-470	Sequence 2691, Ap
38	16	59.3	1245	4	US-09-134-001C-2691	Sequence 3, Appli
39	16	59.3	3490	2	US-08-841-483-3	Sequence 3, Appli
40	16	59.3	3490	2	US-09-382-911-3	Sequence 5, Appli
41	16	59.3	4094	2	US-08-841-483-5	Sequence 1267, Ap
42	16	59.3	4094	2	US-09-382-911-5	Sequence 1, Appli
43	15.8	58.5	1194	4	US-09-134-001C-1267	Sequence 11, Appl
44	15.8	58.5	1261	3	US-08-967-272-1	
45	15.8	58.5	2832	4	US-08-476-515A-11	

ALIGNMENTS

RESULT 1

US-09-164-034B-1

GENERAL INFORMATION:

APPLICANT: Mincheff, Milcho S.

Loukinov, I. Dmitri

Zoubak, Serquei

TITLE OF INVENTION: Immunotherapy of Cancer Through Expression

of Truncated Tumor- or Tumor-Associated Antigen

NUMBER OF SEQUENCES: 1

CORRESPONDENCE ADDRESS:

ADDRESSEE: William S. Ramsey,

Ramsey, Cook, Looper & Kurlander, LLC

STREET: 10420 Little Patuxent Parkway, Suite 250

CITY: Columbia

STATE: Maryland

COUNTRY: USA

ZIP: 21044

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage

COMPUTER: PC

OPERATING SYSTEM: Windows 95

SOFTWARE: WordPerfect 8

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/164,034B

FILING DATE: 30-Sep-1998

ATTORNEY/AGENT INFORMATION:

NAME: Ramsey, William S.

REGISTRATION NUMBER: 32,715

REFERENCE/DOCKET NUMBER: bril

TELECOMMUNICATION INFORMATION:

TELEPHONE: (410) 992-9660

TELEFAX: (410) 992-9540

SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-09-164-034B-1

Query Match 100.0%; Score 27; DB 4; Length 2133;

Best Local Similarity 100.0%; Pred. No. 0.001;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGATGTACAGCTTGGTACACACCTTA 27

|||||

Db 1279 CTGATGTACAGCTTGGTACACACCTTA 1305

RESULT 2

US-08-325-553-1

Sequence 1, Application US/08325553

Patent No. 5538866

GENERAL INFORMATION:

APPLICANT: Israeli, Ron S.

APPLICANT: Heston, Warren D.W.  
APPLICANT: Fair, William R.  
TITLE OF INVENTION: THE PROSTATE-SPECIFIC MEMBRANE ANTIGEN  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cooper & Dunham  
STREET: 30 Rockefeller Plaza  
CITY: New York  
STATE: New York  
COUNTRY: United States of America  
ZIP: 10112  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/325,553  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/973,337A  
FILING DATE: 05 NOV 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 1747/41426  
TELEPHONE: (212) 977-9550  
TELEFAX: (212) 664-0525  
TELEX: 422523 COOP UI  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2653 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
TISSUE TYPE: Carcinoma  
IMMEDIATE SOURCE:  
CLONE: Prostate-Specific Membrane Antigen  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 262..2511  
US-08-325-553-1

Query Match 100.0%; Score 27; DB 1; Length 2653;  
Best Local Similarity 100.0%; Pred. No. 0.0011;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGATGACAGCTTGGTACACACCTA 27  
|||||  
Db 1666 CTGATGACAGCTTGGTACACACCTA 1692

RESULT 3  
US-08-394-152A-1  
Sequence 1, Application US/08394152A  
Patent No. 5935818  
GENERAL INFORMATION:  
APPLICANT: Israeli, Ron S.  
APPLICANT: Heston, Warren D.W.  
APPLICANT: Fair, William R.  
TITLE OF INVENTION: PROSTATE-SPECIFIC MEMBRANE ANTIGEN AND  
TITLE OF INVENTION: USES THEREOF  
NUMBER OF SEQUENCES: 48  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cooper & Dunham LLP  
STREET: 1185 Avenue of the Americas

CITY: New York  
STATE: New York  
COUNTRY: United States of America  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM 330 466 DX2  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/394,152A  
FILING DATE: 24-FEB-95  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 41426-B  
TELEPHONE: (212) 278-0400  
TELEFAX: (212) 391-0525  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2653 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
TISSUE TYPE: Carcinoma  
IMMEDIATE SOURCE:  
CLONE: Prostate-Specific Membrane Antigen  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 262..2511  
US-08-394-152A-1

Query Match 100.0%; Score 27; DB 2; Length 2653;  
Best Local Similarity 100.0%; Pred. No. 0.0011;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGATGACAGCTTGGTACACACCTA 27  
|||||  
Db 1666 CTGATGACAGCTTGGTACACACCTA 1692

RESULT 4  
US-08-652-971-1  
Sequence 1, Application US/08652971  
Patent No. 5814507  
GENERAL INFORMATION:  
APPLICANT: Cheng, Jill  
APPLICANT: Lasky, Laurence A.  
TITLE OF INVENTION: A NOVEL KAPPA/MU-LIKE PROTEIN TYROSINE  
TITLE OF INVENTION: PHOSPHATASE, PTP LAMBDA  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd.  
CITY: South San Francisco  
STATE: California  
COUNTRY: United States  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/652,971  
FILING DATE:

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 14, 2003, 13:13:08 ; Search time 33.6667 Seconds  
(without alignments)  
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Title: US-09-821-734-15

Perfect score: 27  
Sequence: 1 ctgatgtacagcttggtacacaccta 27

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 593429 seqs, 438583890 residues

Total number of hits satisfying chosen parameters: 1186858

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications\_NA.\*

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- 2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq.\*
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- 12: /cgn2\_6/ptodata/1/pubpna/US10\_PUBCOMB.seq.\*
- 13: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq.\*
- 14: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	27	100.0	2558	9	US-09-978-295A-617
4	27	100.0	2558	9	US-09-978-697-617
5	27	100.0	2558	9	US-09-978-192A-617
6	27	100.0	2558	9	US-09-999-832A-617
7	27	100.0	2558	9	US-09-978-189-617
8	27	100.0	2558	9	US-10-174-590-103
9	27	100.0	2558	9	US-10-176-758-103
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11	27	100.0	2558	9	US-10-173-706-103
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17	27	100.0	2558	9	US-10-180-552-103
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20	27	100.0	2558	9	US-10-174-572-103	Sequence 103, App
21	27	100.0	2558	9	US-10-174-579-103	Sequence 103, App
22	27	100.0	2558	9	US-10-174-582-103	Sequence 103, App
23	27	100.0	2558	9	US-10-174-588-103	Sequence 103, App
24	27	100.0	2558	9	US-10-175-739-103	Sequence 103, App
25	27	100.0	2558	9	US-10-175-740-103	Sequence 103, App
26	27	100.0	2558	9	US-10-175-743-103	Sequence 103, App
27	27	100.0	2558	9	US-10-176-488-103	Sequence 103, App
28	27	100.0	2558	9	US-10-176-492-103	Sequence 103, App
29	27	100.0	2558	9	US-10-176-747-103	Sequence 103, App
30	27	100.0	2558	9	US-10-176-750-103	Sequence 103, App
31	27	100.0	2558	9	US-10-176-985-103	Sequence 103, App
32	27	100.0	2558	9	US-10-176-987-103	Sequence 103, App
33	27	100.0	2558	9	US-10-176-991-103	Sequence 103, App
34	27	100.0	2558	9	US-10-176-992-103	Sequence 103, App
35	27	100.0	2558	9	US-10-176-993-103	Sequence 103, App
36	27	100.0	2558	9	US-10-184-658-103	Sequence 103, App
37	27	100.0	2558	9	US-10-173-695-103	Sequence 103, App
38	27	100.0	2558	9	US-10-173-697-103	Sequence 103, App
39	27	100.0	2558	9	US-10-173-705-103	Sequence 103, App
40	27	100.0	2558	9	US-10-174-576-103	Sequence 103, App
41	27	100.0	2558	9	US-10-174-585-103	Sequence 103, App
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43	27	100.0	2558	9	US-10-175-747-103	Sequence 103, App
44	27	100.0	2558	9	US-10-176-481-103	Sequence 103, App
45	27	100.0	2558	9	US-10-176-485-103	Sequence 103, App

ALIGNMENTS

RESULT 1  
US-09-821-734-15  
; Sequence 15, Application US/09821734  
; Publication No. US20030027246A1  
; GENERAL INFORMATION:  
; APPLICANT: Chong, Pele  
; APPLICANT: Pedyczak, Artur  
; APPLICANT: Sia, Charles Dwo Yuan  
; TITLE OF INVENTION: Immunogenic Peptides Derived from Prostate-Specific Membrane  
; TITLE OF INVENTION: (PSMA) and Uses Thereof  
; FILE REFERENCE: 11014-22  
; CURRENT APPLICATION NUMBER: US/09/821,734  
; CURRENT FILING DATE: 2001-03-30  
; PRIOR APPLICATION NUMBER: US 60/193,386  
; PRIOR FILING DATE: 2000-03-31  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 15  
; LENGTH: 27  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: CLP333  
US-09-821-734-15

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Best Local Similarity 100.0%; Pred. No. 0.0013;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 CTGATGTACAGCTTGGTACACACCTA 27

RESULT 2  
US-09-925-300-86  
; Sequence 86, Application US/09925300  
; Patent No. US20020151681A1  
; GENERAL INFORMATION:  
; APPLICANT: Craig Rosen,  
; APPLICANT: Steve Ruben  
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

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FILE REFERENCE: PA101
CURRENT APPLICATION NUMBER: US/09/925,300
PRIOR FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05988
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1890
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 86
LENGTH: 1037
TYPE: DNA
ORGANISM: Homo sapiens
US-09-925-300-86

Query Match      100.0%; Score 27; DB 10; Length 1037;
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Db 53 CTCGATGACGCTGGTACACACCTA 79

RESULT 3
US-09-978-295A-617
Sequence 617, Application US/09978295A
Patent No. US20020156006A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnovers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austlin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C11
CURRENT APPLICATION NUMBER: US/09/978,295A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
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PRIOR FILING DATE: 1998-03-11
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PRIOR FILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 60/078004
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PRIOR APPLICATION NUMBER: 60/078939
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
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PRIOR FILING DATE: 1998-03-27
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PRIOR FILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 60/079923
PRIOR FILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 60/080105
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080107
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080165
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080194
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080327
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080328
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080333
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080334
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/081070
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081049
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081071
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081195
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081203
PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081229
PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081955
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081817
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081819
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081952
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081838
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GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

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Run on: April 14, 2003, 09:33:49 ; Search time 828.5 Seconds

(without alignments)  
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Title: US-09-821-734-15

Perfect score: 27

Sequence: 1 ctgtgtacagcttggtacacacctta 27

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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3: em\_estlin:\*

4: em\_estmu:\*

5: em\_estov:\*

6: em\_estpl:\*

7: em\_estro:\*

8: em\_htc:\*

9: gb\_estli:\*

10: gb\_est2:\*

11: gb\_htc:\*

12: gb\_est3:\*

13: gb\_est4:\*

14: gb\_est5:\*

15: em\_estfun:\*

16: em\_estom:\*

17: gb\_gss:\*

18: em\_gss\_hum:\*

19: em\_gss\_inv:\*

20: em\_gss\_pln:\*

21: em\_gss\_vrt:\*

22: em\_gss\_fun:\*

23: em\_gss\_mam:\*

24: em\_gss\_mus:\*

25: em\_gss\_Other:\*

26: em\_gss\_pro:\*

27: em\_gss\_rod:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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2	27	100.0	474	10	AW945136
3	27	100.0	563	10	AW951407
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5	27	100.0	767	12	BG194269
6	27	100.0	938	9	AL532732

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C	8	22.2	82.2	459	9	AI892895
C	9	22.2	82.2	464	9	AI647690
C	10	22.2	82.2	662	9	AA116793
C	11	22.2	82.2	3003	11	AK002920
C	12	20.6	76.3	278	9	AI788531
C	13	19.6	72.6	874	13	BG831345
C	14	19.6	72.6	874	13	BI908012
C	15	19.2	71.1	610	17	FR0028442
C	16	19.2	71.1	653	17	CNS07600
C	17	19.2	71.1	705	17	BH176186
C	18	19.2	71.1	705	17	CNS07305
C	19	19.2	71.1	710	10	AV979798
C	20	19	70.4	527	13	BJ221163
C	21	18.8	69.6	536	10	BB728352
C	22	18.8	69.6	1289	14	BQ718347
C	23	18.6	68.9	400	9	AL837844
C	24	18.6	68.9	435	13	BJ074589
C	25	18.6	68.9	457	17	AQ812530
C	26	18.6	68.9	460	17	AQ513855
C	27	18.6	68.9	514	13	BJ061531
C	28	18.6	68.9	514	13	BJ066254
C	29	18.6	68.9	554	13	BJ061747
C	30	18.6	68.9	566	13	BJ052567
C	31	18.6	68.9	583	10	BE192345
C	32	18.6	68.9	594	10	AV951122
C	33	18.6	68.9	594	13	BJ064305
C	34	18.6	68.9	630	13	BJ096767
C	35	18.6	68.9	636	13	BJ072058
C	36	18.6	68.9	639	13	BJ074118
C	37	18.6	68.9	649	17	BH277517
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C	39	18.6	68.9	923	14	BQ724752
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C	41	18.4	68.1	889	9	AI788829
C	42	18.2	67.4	253	10	AW317248
C	43	18.2	67.4	344	12	BG873877
C	44	18.2	67.4	612	9	AL634736
C	45	18.2	67.4	638	14	BQ522172

# ALIGNMENTS

RESULT 1	AA371450	296 bp	mRNA	linear	EST 21-APR-1997
LOCUS	EST83235	Prostate gland I	Homo sapiens	cDNA 5' end similar to	
DEFINITION	prostate-specific membrane antigen, mRNA sequence.				
ACCESSION	AA371450				
VERSION	AA371450.1	GI:2023767			
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Euthera; Primates; Catarrhini; Hominoidea; Homo.				
AUTHORS	1 (bases 1 to 296)				
	Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A., Bult				
	,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., White				
	,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C., Clayton,R.A.,				
	Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald				
	,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S., Gloddek,A.,				
	Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr., Kelley,J.M.,				
	Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,				
	Morono-Palancas,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,				
	Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,				
	Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,				
	Bednarek,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,				
	Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A., He,W.W.				
	,Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L.,				
	Kunsch,C., Hungjun,J., Li,H., Weissner,P.S., Olsen,H., Raymond,L.,				
	Wei,X.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., Dillion,P.J., Fannon				
	,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and				

Venter, J.C.  
Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence  
Nature 377 (6547 Suppl), 3-174 (1995)  
96026280  
Other\_ESTs: THC166946  
Contact: Kerlavage, AR  
Bioinformatics  
The Institute for Genomic Research  
9712 Medical Center Drive, Rockville, MD 20850 USA  
Tel: 3018699056  
Fax: 3018699423  
Email: arkerlavet@tigr.org  
For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (<http://www.tigr.org/tdb/hgl/hgl1.html>)  
Seq primer: M13 Reverse.

## FEATURES

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Location/Qualifiers

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/db\_xref="taxon:9606"

/clone\_lib="Prostate gland I"

/sex="male"

/dev\_stage="adult, 21 yrs"

/note="Organ: prostate; Vector: pBluescript SK-; Site\_1:

EcoRI; Site\_2: XhoI"

BASE COUNT 98 a 58 c 66 g 73 t 1 others

## ORIGIN

Query Match 100.0%; Score 27; DB 9; Length 296;  
Best Local Similarity 100.0%; Pred. No. 0.066;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 53 CTGATGTACAGCTTGGTACACACCTA 79

## RESULT 2

AW945136

LOCUS

EST361329 MAGE resequences, MAGA Homo sapiens cDNA, mRNA sequence. EST 31-MAY-2000

ACCESSION AW945136

VERSION AW945136.1 GI:8122887

KEYWORDS

EST.

SOURCE

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 474)

Hegde, P., Qi, R., Abernathy, K., Dharap, S., Gaspard, R., Gay, C., Holt

, I.E., Saeed, A.I., Sharov, V., Lee, N.H., Yeatman, T.J. and

Quackenbush, J.

Assessment of gene expression patterns in a model of colon tumor

metastasis using a 19,200 element cDNA microarray

Unpublished (2000)

Contact: John Quackenbush

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 3528

Fax: 301 838 0208

Email: johnq@tigr.org

Plate: 0

Seq primer: Reverse.

Location/Qualifiers

1..474

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone\_lib="MAGE resequences, MAGA"

/note="Vector: pBluescriptSKm"

BASE COUNT 145 a 79 c 84 g 166 t

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Best Local Similarity 100.0%; Pred. No. 0.076;  
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Db 52 CTGATGTACAGCTTGGTACACACCTA 78

## RESULT 3

AW951407

LOCUS

EST363477 MAGE resequences, MAGB Homo sapiens cDNA, mRNA sequence. EST 01-JUN-2000

ACCESSION AW951407

VERSION AW951407.1 GI:8141080

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 563)

Hegde, P., Qi, R., Abernathy, K., Dharap, S., Gaspard, R., Gay, C., Holt

, I.E., Saeed, A.I., Sharov, V., Lee, N.H., Yeatman, T.J. and

Quackenbush, J.

Assessment of gene expression patterns in a model of colon tumor

metastasis using a 19,200 element cDNA microarray

Unpublished (2000)

Contact: John Quackenbush

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 3528

Fax: 301 838 0208

Email: johnq@tigr.org

Plate: 27

Seq primer: Reverse.

Location/Qualifiers

1..563

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone\_lib="MAGE resequences, MAGB"

/note="Vector: pBluescriptSKm"

BASE COUNT 179 a 102 c 121 g 160 t 1 others

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0.08;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGATGTACAGCTTGGTACACACCTA 27

|||||

Db 52 CTGATGTACAGCTTGGTACACACCTA 78

## RESULT 4

BG206102

LOCUS

R525537 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence. EST 21-APR-2001

ACCESSION BG206102

VERSION BG206102.1 GI:13727789

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 625)

Harrington, J.J., Sherf, B., Rundlett, S., Jackson, P.D., Perry, R.,

Cain, S., Leventhal, C., Thornton, M., Ramchandran, R., Whittington, J.

, Lerner, L., Costanzo, D., McElligott, K., Booser, S., Mays, R., Smith

, E., Veloso, N., Klika, A., Hess, J., Cothren, K., Lo, K., Offenbacher

, J., Danzig, J. and Ducar, M.

Creation of genome-wide protein expression libraries using random

activation of gene expression



GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 14, 2003, 09:31:34 ; Search time 523.667 Seconds  
(without alignments)  
1500.527 Million cell updates/sec

Title: US-09-821-734-16  
Perfect score: 27  
Sequence: 1 atgatgaatgatcaactcatgtttctg 27

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues  
Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

GenEmbl.\*

- 1: gb\_ba.\*
- 2: gb\_htg.\*
- 3: gb\_in.\*
- 4: gb\_on.\*
- 5: gb\_ov.\*
- 6: gb\_pat.\*
- 7: gb\_ph.\*
- 8: gb\_pl.\*
- 9: gb\_pr.\*
- 10: gb\_ro.\*
- 11: gb\_sts.\*
- 12: gb\_sy.\*
- 13: gb\_un.\*
- 14: gb\_vi.\*
- 15: em\_ba.\*
- 16: em\_fun.\*
- 17: em\_hum.\*
- 18: em\_in.\*
- 19: em\_mu.\*
- 20: em\_on.\*
- 21: em\_or.\*
- 22: em\_ov.\*
- 23: em\_pat.\*
- 24: em\_ph.\*
- 25: em\_pl.\*
- 26: em\_ro.\*
- 27: em\_sts.\*
- 28: em\_un.\*
- 29: em\_vi.\*
- 30: em\_htg\_hum.\*
- 31: em\_htg\_inv.\*
- 32: em\_htg\_other.\*
- 33: em\_htg\_mus.\*
- 34: em\_htg\_pln.\*
- 35: em\_htg\_rod.\*
- 36: em\_htg\_mam.\*
- 37: em\_htg\_vrt.\*
- 38: em\_sy.\*
- 39: em\_htgo\_hum.\*
- 40: em\_htgo\_mus.\*
- 41: em\_htgo\_other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	27	100.0	27	6	AX268378	Sequence
2	27	100.0	1992	9	AF261715	Homo sapi
3	27	100.0	2061	6	AX403107	Sequence
4	27	100.0	2253	6	AX467227	Sequence
5	27	100.0	2253	9	AY101595	Homo sapi
6	27	100.0	2518	9	AF176574	Homo sapi
7	27	100.0	2558	6	AX376036	Sequence
8	27	100.0	2653	6	AX337498	Sequence
9	27	100.0	2653	6	123794	Sequence 1
10	27	100.0	2653	9	HUMPSM	Human prost
11	27	100.0	67466	2	AC103729	Homo sapi
12	27	100.0	67466	2	AC103729	Homo sapi
13	27	100.0	93525	9	AF007544	Homo sapi
14	27	100.0	137888	9	AF003122	Homo sapi
15	27	100.0	156255	2	AP002369	Homo sapi
16	27	100.0	157527	9	AC117746	Homo sapi
17	27	100.0	158524	2	AL162372	Homo sapi
18	27	100.0	187638	2	AC118273	Homo sapi
19	27	100.0	192648	2	AC024234	Homo sapi
20	27	100.0	246865	2	AC074003	Homo sapi
21	23.8	88.1	170102	9	AC009237	Homo sapi
22	22.2	82.2	2532	4	AF050502	Sus scrofa
23	21.8	80.7	66084	8	AB015468	Arabidops
24	21.2	78.5	73794	2	AC101544	Mus muscu
25	21.2	78.5	182240	2	AC131039	Mus muscu
26	20.8	77.0	180812	2	AC127403	Rattus no
27	20.6	76.3	3152	6	AX006438	Sequence
28	20.6	76.3	3152	9	HSA012370	Homo sapi
29	20.6	76.3	3171	6	AX136153	Sequence
30	20.6	76.3	91667	2	AP005435	Homo sapi
31	20.6	76.3	120000	9	AP004607	Homo sapi
32	20.6	76.3	149745	9	AP000648	Homo sapi
33	20.6	76.3	166287	2	AC060830	Homo sapi
34	20.6	76.3	168577	9	AP000827	Homo sapi
35	20.6	76.3	173005	2	AP001769	Homo sapi
36	20.6	76.3	189711	2	AC096944	Rattus no
37	20.4	75.6	241280	2	AC020854	Mus muscu
38	20.2	74.8	112375	2	AC120576	Rattus no
39	20.2	74.8	113939	2	AP004052	Oryza sat
40	20.2	74.8	122241	2	AP004129	Oryza sat
41	20.2	74.8	150927	2	AP004756	Oryza sat
42	20.2	74.8	182520	2	AC112304	Rattus no
43	20.2	74.8	211023	2	AL807239	Danio rer
44	19.8	73.3	106376	9	AL138714	Human DNA
45	19.8	73.3	156806	2	AC021353	Homo sapi

ALIGNMENTS

RESULT 1	AX268378	Sequence 16 from Patent WO0174845.	27 bp	DNA	linear	PAT 29-OCT-2001
LOCUS	AX268378	Sequence 16 from Patent WO0174845.	27 bp	DNA	linear	PAT 29-OCT-2001
DEFINITION	AX268378	Sequence 16 from Patent WO0174845.	27 bp	DNA	linear	PAT 29-OCT-2001
ACCESSION	AX268378	Sequence 16 from Patent WO0174845.	27 bp	DNA	linear	PAT 29-OCT-2001
VERSION	AX268378.1	GI:16541585				
KEYWORDS		synthetic construct.				
SOURCE		synthetic construct.				
ORGANISM		artificial sequences.				
REFERENCE		1				
AUTHORS		Pedyczak A., Chong P. and Sia C.D.				
TITLE		Immunogenic peptides derived from prostate-specific membrane antigen (psma) and uses thereof				
JOURNAL		Patent: WO 01/74845-A 16 11-OCT-2001;				

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 /note="CLP336"  
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 Best Local Similarity 100.0%; Pred. No. 0.32; 0; Indels 0; Gaps 0;  
 Matches 27; Conservative 0; Mismatches 0;  
**QY** 1 ATGATGAATGATCACTCATGTTTCTG 27  
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**DB** 1 ATGATGAATGATCACTCATGTTTCTG 27  
 |||||  
**RESULT 2**  
**LOCUS** AF261715 1992 bp mRNA linear PRI 02-NOV-2000  
**DEFINITION** Homo sapiens prostate-specific membrane antigen-like protein  
 (PSMAL/GCP III) mRNA, complete cds.  
**ACCESSION** AF261715  
**VERSION** AF261715.1 GI:11078563  
**KEYWORDS**  
**SOURCE** Homo sapiens.  
**ORGANISM** Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
**REFERENCE**  
**AUTHORS** O'Keefe, D.S., Bacich, D.J. and Heston, W.D.W.  
**TITLE** Cloning and Characterization of a novel glutamate-preferring  
 peptidase that maps to the SCZDII locus: a candidate gene for  
 Schizophrenia?  
**JOURNAL** Unpublished  
**REFERENCE** 2 (bases 1 to 1992)  
**AUTHORS** O'Keefe, D.S., Bacich, D.J. and Heston, W.D.W.  
**TITLE** Expression Profile of Prostate-Specific Membrane Antigen (PSMA)  
 versus a Prostate-Specific Membrane Antigen-Like Gene in Normal  
 Tissues, Prostate Cancer and Tumor Associated-Vasculature  
 Unpublished  
**JOURNAL** 3 (bases 1 to 1992)  
**AUTHORS** O'Keefe, D.S., Bacich, D.J. and Heston, W.D.W.  
**TITLE** Direct Submission  
**JOURNAL** Submitted (27-APR-2000) Cancer Biology, Cleveland Clinic  
 Foundation, NB 40, 9500 Euclid Avenue, Cleveland, OH 44195, USA  
**FEATURES**  
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 1. .1992  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /chromosome="11"  
 /map="11q14.3"  
 /tissue\_type="liver"  
 /note="maps to Schizophrenia Disorder Type II locus"  
 1. .1992  
 /gene="PSMAL/GCP III"  
 527. .1855  
 /gene="PSMAL/GCP III"  
 /function="N-acetylated-alpha-linked-acidic dipeptidase"  
 /note="glutamate carboxypeptidase III; similar to Homo  
 sapiens PSMA; folate hydrolase-like; member of the M28  
 peptidase family; formed by duplication of the PSMA gene"  
 /codon\_start=1  
 /product="prostate-specific membrane antigen-like protein"  
 /protein\_id="AAC29102.1"  
 /db\_xref="GI:11078564"  
 /translation="MGSAAPPDSSWRGSLKVSYNVGFSTQKVMHIHSTNEV  
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 LMYSLVNTLKLKSPDEGCKGSLVSKTSKSPSPFSGMPSRISKLGSNGDFEVPFQ  
 RLGIASGRARYTKNWEKNFSGCYPLVSHVYETVELKFDPMFKYHLTVAVQRGVM  
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**DB** 1589 ATGATGAATGATCACTCATGTTTCTG 1615  
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**RESULT 3**  
**LOCUS** AX403107 2061 bp DNA linear PAT 07-JUN-2002  
**DEFINITION** Sequence 2 from Patent WO0226984.  
**ACCESSION** AX403107  
**VERSION** AX403107.1 GI:21388049  
**KEYWORDS**  
**SOURCE** human.  
**ORGANISM** Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
**REFERENCE**  
**AUTHORS** Betty, M., An, W., Ling, H.P. and Rhodes, K.  
**TITLE** Potassium channel interactors and uses therefor  
 Patent: WO 0226984-A 2 04-APR-2002;  
 MILLENNIUM PHARM INC (US)  
**FEATURES**  
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 1. .2061  
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**RESULT 4**  
**LOCUS** AX467227 2253 bp DNA linear PAT 16-JUL-2002  
**DEFINITION** Sequence 1 from Patent WO0234287.  
**ACCESSION** AX467227  
**VERSION** AX467227.1 GI:21900509  
**KEYWORDS**  
**SOURCE** human.  
**ORGANISM** Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
**REFERENCE**  
**AUTHORS** Beier, A.M., Gautam, A. and Mouritsen, S.R.  
**TITLE** Novel therapeutic vaccine formulations  
 Patent: WO 0234287-A 1 02-MAY-2002;  
 Pharmexa A/S (DK)  
**FEATURES**  
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GenCore version 5.1.3  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 14, 2003, 09:27:29 ; Search time 99 Seconds  
(without alignments)  
614.181 Million cell updates/sec

Title: US-09-821-734-16  
Perfect score: 27  
Sequence: 1 atgatgaatgatcaactcatgtttctg 27

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Result No.	Score	Query Match	Length	ID	Description
1	27	100.0	27	AA151143	Human DNA encoding
2	27	100.0	442	ABK64577	Human benign prost
3	27	100.0	578	ABV43616	Human prostate exp
4	27	100.0	1037	AAFI5651	Human prostate can
5	27	100.0	1992	AAAC61762	cdNA encoding a pr
6	27	100.0	2061	AAAC34009	Human gene 4 cdNA
7	27	100.0	2226	AAAI2732	DNA encoding a hum
8	27	100.0	2253	AAAO9454	Human prostate spe
9	27	100.0	2558	AAK78599	Human PRO739 nucle

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

10	27	100.0	2558	22	AA545976	Human DNA encoding
11	27	100.0	2653	15	AAQ65520	Prostate-specific
12	27	100.0	2653	24	ABK66204	cdNA encoding huma
13	27	100.0	2653	24	ABK64556	Human benign prost
14	27	100.0	2653	24	ABL69670	Prostate cancer re
15	27	100.0	2654	17	AA136785	Prostate-specific
16	27	100.0	2884	23	ABV22873	Human prostate exp
17	27	100.0	2884	23	ABV23013	Human prostate exp
18	27	100.0	2884	23	ABV28703	Human prostate exp
19	27	100.0	2884	23	ABV28849	Human prostate exp
20	20.6	76.3	3110	21	AA258312	Human peptidase NA
21	20.6	76.3	3171	22	AA193781	Human cdNA encodin
22	20.6	76.3	3771	22	AAH98667	Human EST-derived
23	19	70.4	249	24	ABL72340	Corn tassal-derive
24	19	70.4	678	24	ABN90915	Staphylococcus epi
25	19	70.4	723	24	ABK15070	Potato cdNA for hi
26	19	70.4	2082	21	AAA09459	Murine prostate sp
27	19	70.4	2256	21	AAA09458	Murine prostate sp
28	18.6	68.9	693	22	AAH04248	Human cdNA clone (
29	18.6	68.9	719	22	AAH30470	DNA encoding novel
30	18.6	68.9	719	22	AAH06250	Human reproductive
31	18.6	68.9	753	11	AAQ05733	Glutathione-S-tran
32	18.6	68.9	1862	22	AAH17257	Human cdNA sequenc
33	18.6	68.9	2548	21	AA235758	Strongylocentrotus
34	18.6	68.9	24789	23	ABL28640	Drosophila melanog
35	18.6	68.9	130480	22	AAF25833	R. marinus bacteri
36	18.4	68.1	16532	23	ABLI2290	Drosophila melanog
37	18.2	67.4	910715	20	AAK20248	Borrelia burgdorfe
38	18	66.7	27	22	AA151149	Human DNA encoding
39	18	66.7	300	21	AAA00166	Human colon cancer
40	18	66.7	354	21	AAK18682	Human secreted pro
41	18	66.7	368	24	ABQ85523	Arabidopsis thalia
42	18	66.7	475	22	ABA52291	Human foetal liver
43	18	66.7	475	22	ABA22092	Probe #558 for gen
44	18	66.7	475	22	AAK00566	Human brain expres
45	18	66.7	475	22	AAK26015	Human bone marrow

#### ALIGNMENTS

RESULT 1  
AA151143  
ID AA151143 standard; DNA; 27 BP.

XX AA151143;

XX 16-JAN-2002 (first entry)

XX Human DNA encoding a PSMA derived immunogenic peptide CLP336.

XX Human; ds; PSMA; prostate specific membrane antigen; prostate cancer;  
tumour; immunogenic peptide; cytostatic; gene therapy; CLP336.

XX Homo sapiens.

XX Key Location/Qualifiers

XX CDS 1..27

XX /tag= a

XX /product= "CLP336"

XX /partial

XX /note= "No stop codon"

XX WO200174845-A2.

XX 11-OCT-2001.

XX 30-MAR-2001; 2001WO-CA00411.

XX 31-MAR-2000; 2000US-193386P.

XX (AVET ) AVENTIS PASTEUR LTD.

PI Pedyczak A, Chong P, Sia CDY;  
 XX WPI; 2001-626378/72.  
 DR P-PSDB; AAU09108.  
 XX  
 PT New polypeptides useful for inducing an immune response and treating  
 PT prostate cancer comprises polypeptides derived from the prostate  
 PT specific membrane antigen -  
 XX  
 XX Claim 6; Page 15; 47pp; English.  
 XX  
 CC The invention relates to prostate specific membrane antigen (PSMA)  
 CC derived peptides (and the nucleic acids encoding them) capable of  
 CC eliciting an immune response. The molecules of the invention are used to  
 CC elicit an immune response, particularly to treat cancer and tumours,  
 CC especially prostate cancer. Delivery of the peptides may be by  
 CC expression from the nucleic acids encoding them (i.e. gene therapy).  
 CC The present sequence encodes a PSMA derived immunogenic peptide.  
 XX  
 XX Sequence 27 BP; 8 A; 4 C; 5 G; 10 T; 0 other;  
 SQ  
 Query Match 100.0%; Score 27; DB 22; Length 27;  
 Best Local Similarity 100.0%; Pred. No. 0.016;  
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ATGATGAATGATCAACTCATGTTTCTG 27  
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 DB 1 ATGATGAATGATCAACTCATGTTTCTG 27  
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 ABK64577/c  
 ID ABK64577 standard; DNA; 442 BP.  
 XX  
 AC ABK64577;  
 XX  
 XX 18-JUN-2002 (first entry)  
 DT  
 DE Human benign prostatic hyperplasia gene #472.  
 XX  
 KW Human; benign prostatic hyperplasia; BPH; prostate cancer; gene; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200212440-A2.  
 XX  
 XX 14-FEB-2002.  
 PD  
 XX 07-AUG-2001; 2001WO-US24708.  
 PF  
 XX 07-AUG-2000; 2000US-223323P.  
 PR 05-JUN-2001; 2001US-0873319.  
 XX  
 XX (GENE-) GENE LOGIC INC.  
 PA (NIBS ) JAPAN TOBACCO INC.  
 XX  
 XX Munger WE, Kulkarni P, Getzenberg RH, Waga I, Yamamoto J;  
 PI WPI; 2002-257476/30.  
 XX  
 DR Identifying drugs for and diagnosing benign prostatic hyperplasia, by  
 XX detecting expression levels of one or more genes in prostate cells from  
 PT patient that are differentially regulated compared to normal prostate  
 PT cells -  
 PT  
 XX Disclosure; Page 274; 444pp; English.  
 PS  
 XX The invention relates to a method of diagnosing (I) the onset or  
 CC progression of benign prostatic hyperplasia (BPH), or screening (II) for  
 CC or identifying an agent that modulates the onset or progression of BPH.  
 CC The method is based on changes in gene expression in BPH tissue isolated  
 CC from patients exhibiting different clinical states of prostate  
 CC hyperplasia as compared to normal prostate tissue. (I) comprises

CC detecting the expression levels of one or more genes in prostate cells  
 CC from the subject that are differentially regulated compared to normal  
 CC prostate cells. (II) comprises preparing a first gene expression profile  
 CC of BPH cells or BPH-like cell population, exposing the cells to the  
 CC agent, preparing a second gene expression profile of the agent exposed  
 CC cells, and comparing the first and second gene expression profiles.  
 CC (I) is useful for diagnosing the onset or progression of BPH. (II) is  
 CC useful for identifying an agent that modulates the onset or progression  
 CC of BPH. The methods are useful to present information identifying  
 CC the expression level in a tissue or cells, by comparing the expression  
 CC level of genes given in the specification in the tissue or cells to the  
 CC expression levels of at least one gene in the tissue or cell sample  
 CC compared to the expression level in BPH. Agents using (II) are useful for  
 CC treating BPH or prostate cancer. ABK64106-ABK64860 represent human  
 CC benign prostatic hyperplasia gene sequences of the invention.  
 XX  
 SQ Sequence 442 BP; 127 A; 102 C; 71 G; 142 T; 0 other;  
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 Best Local Similarity 100.0%; Pred. No. 0.024;  
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ATGATGAATGATCAACTCATGTTTCTG 27  
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 DB 385 ATGATGAATGATCAACTCATGTTTCTG 359  
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 ABV43616/c  
 ID ABV43616 standard; cDNA; 578 BP.  
 XX  
 AC ABV43616;  
 XX  
 XX 16-SEP-2002 (first entry)  
 DT  
 DE Human prostate expression marker cDNA 43607.  
 XX  
 KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;  
 KW pharmacogenomic marker; gene; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200160860-A2.  
 XX  
 XX 23-AUG-2001.  
 PD  
 XX 20-FEB-2001; 2001WO-US05171.  
 PF  
 XX 17-FEB-2000; 2000US-183319P.  
 PR 16-MAR-2000; 2000US-189862P.  
 PR 25-MAY-2000; 2000US-207454P.  
 PR 09-JUN-2000; 2000US-211314P.  
 PR 18-JUL-2000; 2000US-219007P.  
 PR 13-DEC-2000; 2000US-255281P.  
 XX  
 XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
 PA  
 XX Schlegel R, Endege WO, Monahan JE;  
 PI WPI; 2001-662795/76.  
 XX  
 DR Novel isolated nucleic acid molecule associated with cancerous state of  
 PT prostate cells and correlating with presence of prostate cancer, useful  
 PT for detecting presence of prostate cancer, stage of prostate cancer -  
 PT  
 XX Claim 1; Page 8684; 11750pp; English.  
 PS  
 XX The invention relates to an isolated nucleic acid molecule: (I) comprising  
 CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the  
 CC specification or its complement. (I) is useful for:  
 CC (a) assessing whether a patient is afflicted with prostate cancer;  
 CC (b) monitoring the progression of prostate cancer in a patient;

GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: April 14, 2003, 10:10:25 ; Search time 21 Seconds  
(without alignments)  
394.299 Million cell updates/sec

Title: US-09-821-734-16  
Perfect score: 27  
Sequence: 1 atgatgaatgacactcatgtttctg 27

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_NA: \*  
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2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq: \*  
3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq: \*  
4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq: \*  
5: /cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq: \*  
6: /cgn2\_6/ptodata/1/ina/backfiles1.seq: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	27	100.0	2133	4	US-09-164-034B-1
2	27	100.0	2653	1	US-08-325-553-1
3	27	100.0	2653	2	US-08-394-152A-1
4	19	70.4	678	4	US-09-134-001C-378
5	18	66.7	600	5	PCT-US93-10418-3
6	18	66.7	735	3	US-09-135-782-3
7	18	66.7	735	3	US-08-193-191-3
8	17.6	65.2	5577	1	US-08-326-117B-1
9	17.6	65.2	5577	3	US-08-982-129-1
10	17.6	65.2	5582	4	US-09-178-176B-1
11	17.6	65.2	5582	4	US-09-457-864-1
12	17.4	64.4	2423	2	US-08-365-486A-25
13	17.4	64.4	2423	4	US-08-880-342-25
14	17.4	64.4	3517	2	US-08-642-406A-20
15	17.4	64.4	3517	3	US-08-434-000A-1
16	17.4	64.4	3517	4	US-09-312-157-1
17	17.4	64.4	3517	4	US-09-199-534-20
18	17.4	64.4	3517	4	US-09-199-534-20
19	17.4	64.4	87350	3	US-08-781-891-79
20	17.4	64.4	87350	4	US-09-791-211-3
21	17	63.0	3016	4	US-09-221-017B-809
22	17	63.0	3134	4	US-09-668-680-1
23	16.6	61.5	484	4	US-09-020-956-53
24	16.6	61.5	484	4	US-09-030-607-53
25	16.6	61.5	484	4	US-09-605-785-53
26	16.6	61.5	484	4	US-09-439-313-53
27	16.6	61.5	484	4	US-09-352-616A-53

C	28	16.6	61.5	484	4	US-09-232-149A-53	Sequence 53, Appl
	29	16.6	61.5	1001	4	US-09-641-638-406	Sequence 406, App
	30	16.6	61.5	1815	4	US-09-353-133-2	Sequence 2, Appli
	31	16.6	61.5	2001	1	US-08-674-168-24	Sequence 24, Appl
	32	16.6	61.5	2001	3	US-08-985-908-10	Sequence 10, Appl
	33	16.6	61.5	2001	3	US-08-852-730-23	Sequence 23, Appl
C	34	16.6	61.5	2885	4	US-09-232-200-56	Sequence 36, Appl
C	35	16.6	61.5	2885	4	US-09-232-200-56	Sequence 56, Appl
C	36	16.6	61.5	2885	4	US-09-232-197-36	Sequence 36, Appl
C	37	16.6	61.5	2885	4	US-09-232-197-36	Sequence 56, Appl
C	38	16.6	61.5	2885	4	US-09-232-201-36	Sequence 36, Appl
C	39	16.6	61.5	2885	4	US-09-232-201-36	Sequence 56, Appl
C	40	16.4	60.7	977	4	US-08-976-259-18	Sequence 18, Appl
C	41	16.4	60.7	1005	2	US-08-761-344-1	Sequence 1, Appli
C	42	16.4	60.7	1239	4	US-08-887-534A-48	Sequence 48, Appl
C	43	16.4	60.7	1239	4	US-08-887-534A-86	Sequence 86, Appl
C	44	16.4	60.7	1569	2	US-08-761-344-3	Sequence 3, Appli
C	45	16.4	60.7	1704	3	US-09-125-287-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1  
US-09-164-034B-1  
GENERAL INFORMATION:  
APPLICANT: Mincheff, Milcho S.  
Loukinov, I. Dmitri  
Zoubak, Serguei  
TITLE OF INVENTION: Immunotherapy of Cancer Through Expression  
of Truncated Tumor- or Tumor-Associated Antigen  
NUMBER OF SEQUENCES: 1  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: William S. Ramsey,  
Ramsey, Cook, Cooper & Kurlander, LLC  
STREET: 10420 Little Patuxent Parkway, Suite 250  
CITY: Columbia  
STATE: Maryland  
COUNTRY: USA  
ZIP: 21044  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage  
COMPUTER: PC  
OPERATING SYSTEM: Windows 95  
SOFTWARE: Wordperfect 8  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/164,034B  
FILING DATE: 30-Sep-1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Ramsey, William S.  
REGISTRATION NUMBER: 32,715  
REFERENCE/DOCKET NUMBER: Bril  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (410) 992-9660  
TELEFAX: (410) 992-9540  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-09-164-034B-1  
Query Match 100.0%; Score 27; DB 4; Length 2133;  
Best Local Similarity 100.0%; Pred. No. 0.0035;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 1 ATGATGAATGATCAACTCATGTTTCTG 27  
|||||  
Db 1861 ATGATGAATGATCAACTCATGTTTCTG 1887  
RESULT 2  
US-08-325-553-1  
Sequence 1, Application US/08325553  
Patent No. 5538866  
GENERAL INFORMATION:  
APPLICANT: Israeli, Ron S.

APPLICANT: Heston, Warren D.W.  
APPLICANT: Fair, William R.  
TITLE OF INVENTION: THE PROSTATE-SPECIFIC MEMBRANE ANTIGEN  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cooper & Dunham  
STREET: 30 Rockefeller Plaza  
CITY: New York  
STATE: New York  
COUNTRY: United States of America  
ZIP: 10112  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/325,553  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/973,337A  
FILING DATE: 05 NOV 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 1747/41426  
TELEPHONE: (212) 977-9550  
TELEFAX: (212) 664-0525  
TELEX: 422523 COOP UI  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2653 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
TISSUE TYPE: Carcinoma  
IMMEDIATE SOURCE:  
CLONE: Prostate-Specific Membrane Antigen  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 262..2511  
US-08-325-553-1

Query Match 100.0%; Score 27; DB 1; Length 2653;  
Best Local Similarity 100.0%; Pred. No. 0.0036;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGATGAATGATCAACTCATGTTCTG 27  
|||||  
Db 2248 ATGATGAATGATCAACTCATGTTCTG 2274

RESULT 3  
US-08-394-152A-1  
Sequence 1, Application US/08394152A  
Patent No. 5935818  
GENERAL INFORMATION:  
APPLICANT: Israeli, Ron S.  
APPLICANT: Heston, Warren D.W.  
APPLICANT: Fair, William R.  
TITLE OF INVENTION: PROSTATE-SPECIFIC MEMBRANE ANTIGEN AND  
NUMBER OF SEQUENCES: 48  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cooper & Dunham LLP  
STREET: 1185 Avenue of the Americas

CITY: New York  
STATE: New York  
COUNTRY: United States of America  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM 330 466 DX2  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/394,152A  
FILING DATE: 24-FEB-95  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 41426-B  
TELEPHONE: (212) 278-0400  
TELEFAX: (212) 391-0525  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2653 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
TISSUE TYPE: Carcinoma  
IMMEDIATE SOURCE:  
CLONE: Prostate-Specific Membrane Antigen  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 262..2511  
US-08-394-152A-1

Query Match 100.0%; Score 27; DB 2; Length 2653;  
Best Local Similarity 100.0%; Pred. No. 0.0036;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGATGAATGATCAACTCATGTTCTG 27  
|||||  
Db 2248 ATGATGAATGATCAACTCATGTTCTG 2274

RESULT 4  
US-09-134-001C-378  
Sequence 378, Application US/09134001C  
Patent No. 6380370  
GENERAL INFORMATION:  
APPLICANT: Lynn Doucette-Stamm et al  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS  
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: CTC-007  
CURRENT APPLICATION NUMBER: US/09/134,001C  
CURRENT FILING DATE: 1998-08-13  
PRIOR APPLICATION NUMBER: US 60/064,964  
PRIOR FILING DATE: 1997-11-08  
PRIOR APPLICATION NUMBER: US 60/055,779  
PRIOR FILING DATE: 1997-08-14  
NUMBER OF SEQ ID NOS: 5674  
SEQ ID NO 378  
LENGTH: 678  
TYPE: DNA  
ORGANISM: Staphylococcus epidermidis  
US-09-134-001C-378

Query Match 70.4%; Score 19; DB 4; Length 678;  
Best Local Similarity 81.5%; Pred. No. 9.4;  
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 14, 2003, 13:13:08 ; Search time 33.6667 Seconds  
(without alignments)  
703.471 Million cell updates/sec

Title: US-09-821-734-16  
Perfect score: 27  
Sequence: 1 atgatgaatgacaaactcatgtttctg 27

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 593429 seqs, 43858390 residues 1186858  
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_NA:\*

- 1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:\*
- 2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq:\*
- 3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:\*
- 4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq:\*
- 5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq:\*
- 6: /cgn2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq:\*
- 7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq:\*
- 8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq:\*
- 9: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq:\*
- 10: /cgn2\_6/ptodata/1/pubpna/US09\_PUBCOMB.seq:\*
- 11: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq:\*
- 12: /cgn2\_6/ptodata/1/pubpna/US10\_PUBCOMB.seq:\*
- 13: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*
- 14: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match %	Score	Length	ID	Description
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2	27	100.0	1037	10	US-09-925-300-86
3	27	100.0	2558	9	US-09-978-295A-617
4	27	100.0	2558	9	US-09-978-697-617
5	27	100.0	2558	9	US-09-978-192A-617
6	27	100.0	2558	9	US-09-999-832A-617
7	27	100.0	2558	9	US-09-978-189-617
8	27	100.0	2558	9	US-10-174-590-103
9	27	100.0	2558	9	US-10-176-758-103
10	27	100.0	2558	9	US-10-173-737-103
11	27	100.0	2558	9	US-10-173-706-103
12	27	100.0	2558	9	US-10-175-738-103
13	27	100.0	2558	9	US-10-175-752-103
14	27	100.0	2558	9	US-10-176-482-103
15	27	100.0	2558	9	US-10-176-757-103
16	27	100.0	2558	9	US-10-176-913-103
17	27	100.0	2558	9	US-10-180-552-103
18	27	100.0	2558	9	US-10-180-557-103
19	27	100.0	2558	9	US-10-173-700-103

20	27	100.0	2558	9	US-10-174-572-103	Sequence 103, App
21	27	100.0	2558	9	US-10-174-579-103	Sequence 103, App
22	27	100.0	2558	9	US-10-174-582-103	Sequence 103, App
23	27	100.0	2558	9	US-10-174-588-103	Sequence 103, App
24	27	100.0	2558	9	US-10-175-739-103	Sequence 103, App
25	27	100.0	2558	9	US-10-175-740-103	Sequence 103, App
26	27	100.0	2558	9	US-10-175-743-103	Sequence 103, App
27	27	100.0	2558	9	US-10-176-488-103	Sequence 103, App
28	27	100.0	2558	9	US-10-176-492-103	Sequence 103, App
29	27	100.0	2558	9	US-10-176-747-103	Sequence 103, App
30	27	100.0	2558	9	US-10-176-750-103	Sequence 103, App
31	27	100.0	2558	9	US-10-176-985-103	Sequence 103, App
32	27	100.0	2558	9	US-10-176-987-103	Sequence 103, App
33	27	100.0	2558	9	US-10-176-991-103	Sequence 103, App
34	27	100.0	2558	9	US-10-176-992-103	Sequence 103, App
35	27	100.0	2558	9	US-10-176-993-103	Sequence 103, App
36	27	100.0	2558	9	US-10-184-658-103	Sequence 103, App
37	27	100.0	2558	9	US-10-173-695-103	Sequence 103, App
38	27	100.0	2558	9	US-10-173-697-103	Sequence 103, App
39	27	100.0	2558	9	US-10-173-705-103	Sequence 103, App
40	27	100.0	2558	9	US-10-174-576-103	Sequence 103, App
41	27	100.0	2558	9	US-10-174-585-103	Sequence 103, App
42	27	100.0	2558	9	US-10-174-586-103	Sequence 103, App
43	27	100.0	2558	9	US-10-175-747-103	Sequence 103, App
44	27	100.0	2558	9	US-10-176-481-103	Sequence 103, App
45	27	100.0	2558	9	US-10-176-485-103	Sequence 103, App

ALIGNMENTS

RESULT 1  
US-09-821-734-16  
; Sequence 16, Application US/09821734  
; Publication No. US20030027246A1  
; GENERAL INFORMATION:  
; APPLICANT: Chong, Pele  
; APPLICANT: Pedyczak, Artur  
; APPLICANT: Sia, Charles Dwo Yuan  
; TITLE OF INVENTION: Immunogenic Peptides Derived from Prostate-Specific Membran  
; FILE REFERENCE: (PSMA) and Uses Thereof  
; FILE REFERENCE: 11014-22  
; CURRENT APPLICATION NUMBER: US/09/821,734  
; PRIOR FILING DATE: 2001-03-30  
; PRIOR FILING DATE: 2000-03-31  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 16  
; LENGTH: 27  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: CLP336  
US-09-821-734-16

Query Match 100.0%; Score 27; DB 9; Length 27;  
Best Local Similarity 100.0%; Pred. No. 0.0091;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGATGAATGATCAACTCATGTTTCTG 27  
|||||  
Db 1 ATGATGAATGATCAACTCATGTTTCTG 27

RESULT 2  
US-09-925-300-86  
; Sequence 86, Application US/09925300  
; Patent No. US20020151681A1  
; GENERAL INFORMATION:  
; APPLICANT: Craig Rosen,  
; APPLICANT: Steve Ruben  
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

FILE REFERENCE: PA101  
CURRENT APPLICATION NUMBER: US/09/925,300  
CURRENT FILING DATE: 2001-08-10  
PRIOR APPLICATION NUMBER: PCT/US00/05988  
PRIOR FILING DATE: 2000-03-08  
PRIOR APPLICATION NUMBER: 60/124,270  
PRIOR FILING DATE: 1999-03-12  
NUMBER OF SEQ ID NOS: 1890  
SOFTWARE: PatentIn ver. 2.0  
SEQ ID NO 86  
LENGTH: 1037  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-925-300-86

Query Match 100.0%; Score 27; DB 10; Length 1037;  
Best Local Similarity 100.0%; Pred. No. 0.021;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGATGAATGATCAACTCATGTTTCTG 27  
|||||  
Db 636 ATGATGAATGATCAACTCATGTTTCTG 662

RESULT 3  
US-09-978-295A-617  
Sequence 617, Application US/09978295A  
Patent No. US20020156006A1  
GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2630P1C11  
CURRENT APPLICATION NUMBER: US/09/978,295A  
CURRENT FILING DATE: 2001-10-15  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/064249  
PRIOR FILING DATE: 1997-11-03  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066364  
PRIOR FILING DATE: 1997-11-21  
PRIOR APPLICATION NUMBER: 60/077450  
PRIOR FILING DATE: 1998-03-10

PRIOR APPLICATION NUMBER: 60/077632  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077641  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077649  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077791  
PRIOR FILING DATE: 1998-03-12  
PRIOR APPLICATION NUMBER: 60/078004  
PRIOR FILING DATE: 1998-03-13  
PRIOR APPLICATION NUMBER: 60/078886  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/078936  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/078910  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/078939  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/079294  
PRIOR FILING DATE: 1998-03-25  
PRIOR APPLICATION NUMBER: 60/079656  
PRIOR FILING DATE: 1998-03-26  
PRIOR APPLICATION NUMBER: 60/079664  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/079689  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/079663  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/079728  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/079786  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/079920  
PRIOR FILING DATE: 1998-03-30  
PRIOR APPLICATION NUMBER: 60/079923  
PRIOR FILING DATE: 1998-03-30  
PRIOR APPLICATION NUMBER: 60/080105  
PRIOR FILING DATE: 1998-03-31  
PRIOR APPLICATION NUMBER: 60/080107  
PRIOR FILING DATE: 1998-03-31  
PRIOR APPLICATION NUMBER: 60/080165  
PRIOR FILING DATE: 1998-03-31  
PRIOR APPLICATION NUMBER: 60/080194  
PRIOR FILING DATE: 1998-03-31  
PRIOR APPLICATION NUMBER: 60/080327  
PRIOR FILING DATE: 1998-04-01  
PRIOR APPLICATION NUMBER: 60/080328  
PRIOR FILING DATE: 1998-04-01  
PRIOR APPLICATION NUMBER: 60/080333  
PRIOR FILING DATE: 1998-04-01  
PRIOR APPLICATION NUMBER: 60/080334  
PRIOR FILING DATE: 1998-04-01  
PRIOR APPLICATION NUMBER: 60/081070  
PRIOR FILING DATE: 1998-04-08  
PRIOR APPLICATION NUMBER: 60/081049  
PRIOR FILING DATE: 1998-04-08  
PRIOR APPLICATION NUMBER: 60/081071  
PRIOR FILING DATE: 1998-04-08  
PRIOR APPLICATION NUMBER: 60/081195  
PRIOR FILING DATE: 1998-04-08  
PRIOR APPLICATION NUMBER: 60/081203  
PRIOR FILING DATE: 1998-04-09  
PRIOR APPLICATION NUMBER: 60/081229  
PRIOR FILING DATE: 1998-04-09  
PRIOR APPLICATION NUMBER: 60/081955  
PRIOR FILING DATE: 1998-04-15  
PRIOR APPLICATION NUMBER: 60/081817  
PRIOR FILING DATE: 1998-04-15  
PRIOR APPLICATION NUMBER: 60/081819  
PRIOR FILING DATE: 1998-04-15  
PRIOR APPLICATION NUMBER: 60/081952  
PRIOR FILING DATE: 1998-04-15  
PRIOR APPLICATION NUMBER: 60/081838



GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: April 14, 2003, 09:33:49 ; Search time 828.5 seconds  
(without alignments)  
527.795 Million cell updates/sec

Title: US-09-821-734-16

Perfect score: 27

Sequence: 1 atgatgaatgacaaactcatgtttctg 27

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:\*

1: em\_estba:\*

2: em\_esthum:\*

3: em\_estin:\*

4: em\_estmu:\*

5: em\_estov:\*

6: em\_estpl:\*

7: em\_estro:\*

8: em\_htc:\*

9: gb\_est1:\*

10: gb\_est2:\*

11: gb\_htc:\*

12: gb\_est3:\*

13: gb\_est4:\*

14: gb\_est5:\*

15: em\_estfun:\*

16: em\_estom:\*

17: gb\_gss:\*

18: em\_gss\_hum:\*

19: em\_gss\_inv:\*

20: em\_gss\_pln:\*

21: em\_gss\_vit:\*

22: em\_gss\_fun:\*

23: em\_gss\_mam:\*

24: em\_gss\_mus:\*

25: em\_gss\_Other:\*

26: em\_gss\_pro:\*

27: em\_gss\_rod:\*

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	27	100.0	251	14	T29049 EST66546 Hu
2	27	100.0	426	10	AW000926 wr90e01.x
3	27	100.0	442	14	N48056 yy99c12.s1
4	27	100.0	452	14	N64840 yz31h07.s1
5	27	100.0	471	9	A1356718 qy17a12.x
6	27	100.0	474	9	A1474492 th21d01.x

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

LOCUS	251 bp	mrna	linear	EST 06-SEP-1995
DEFINITION	EST66546 Human prostate gland Homo sapiens cDNA 5' end similar to prostate-specific membrane antigen (Ht:361), mRNA sequence.			
ACCESSION	T29049			
VERSION	T29049.1			
KEYWORDS	EST.			
SOURCE	human.			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.			
AUTHORS	Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A., Bult,C.J., Lee,N., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., White,O., Sutton,G., Blake,J.A., Brandon,R.C., Chiu,M.-W., Clayton,R.A., Cline,R.T., Cotton,M.D., Earle-Hughes,J., Fine,L.D., FitzGerald,L.M., FitzHugh,W.M., Fritchman,J.L., Geoghagen,N.S.M., Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkley,P.S., Kelley,J.M., Klimek,K.M., Kelley,J.C., Liu,L.-I., Marmaro,S.M., Merrick,J.M., Moreno-Palanco,R.F., McDonald,L.A., Nguyen,D.T., Pellegrino,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R., Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y., Beznarik,D.P., Cao,L., Cepeda,M.A., Coleman,I.A., Collins,E.-J., Dimke,D., Feng,P., Ferrie,A., Fischer,C., Hastings,G.A., He,W.-W., Hu,J.-S., Greene,J.M., Gruber,J., Hudson,P., Kim,A., Kozak,D.L., Kunsch,C., Ji,H., Li,H., Weissner,P.S., Olsen,H., Raymond,L., Wei,Y.-F., Wing,J., Xu,C., Yu,G.-L., Ruben,S.M., Dillon,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and			

## ALIGNMENTS

RESULT 1	27	100.0	478	10	AW207840
T29049	27	100.0	492	14	N75691 yv29h07.r1
LOCUS	27	100.0	545	14	BQ027857 UI-H-CO0-
DEFINITION	27	100.0	548	12	BF438644 nab89b03.
ACCESSION	27	100.0	618	9	AI766427 wh49h09.x
VERSION	27	100.0	690	9	AI672408 ty64g12.x
KEYWORDS	27	100.0	720	12	BF940223 nac70c04.
SOURCE	27	100.0	770	9	AI050871 ov47b11.x
ORGANISM	27	100.0	776	12	BG208080 RST27570
REFERENCE	27	100.0	797	12	BG202823 RST22191
AUTHORS	27	100.0	928	9	AL563970 AL563970
	22.2	82.2	420	9	AA879028 nw87e05.s
	22.2	82.2	421	10	AA844493 61072 MAR
	22.2	82.2	462	9	AA897668 oj78c06.s
	22.2	82.2	575	13	BI538496 433844 MA
	22.2	82.2	659	13	BM537110 ba78c03.g
	22.2	82.2	745	13	BI183520 UNL-P-FN
	20.6	76.3	569	12	BF334258 RCI-CT024
	20.6	76.3	801	12	BG185042 RST3980 A
	20.2	74.8	916	17	CNS03L0W
	19.8	73.3	499	9	AI545704
	19.6	72.6	424	17	AO626285
	19.6	72.6	449	9	AI586754
	19.6	72.6	489	9	AL730882
	19.6	72.6	500	14	N51443
	19.6	72.6	523	13	BM265401
	19.6	72.6	732	10	BE314435
	19.6	72.6	841	17	AZ677524 ENTL355TR
	19.6	72.6	891	17	AZ538793 ENTGS66TR
	19.6	72.6	919	17	AZ668675 ENT1189TF
	19.4	71.9	293	9	AU228501
	19.4	71.9	626	17	BH116527
	19.2	71.1	207	9	AA142314
	19.2	71.1	406	17	AO761963
	19.2	71.1	523	14	W95980
	19.2	71.1	526	9	AA050162
	19.2	71.1	531	14	W55581
	19.2	71.1	908	17	CNS05BFM
	19.2	71.1	2103	17	AG068108

Venter, J.C.  
 Initial Assessment of Human Gene Diversity and Expression Patterns  
 Based Upon 83 Million Basepairs of cDNA Sequence  
 Nature 377, 3-174 (1995)  
 MEDLINE 96026280  
 COMMENT  
 Contact: Venter, JC  
 The Institute for Genomic Research  
 932 Clopper Rd, Gaithersburg, MD 20878  
 Tel: 3018699056  
 Fax: 3018699423  
 Email: tdbinfo@tdb.tigr.org  
 For clone availability, additional sequence and expression  
 information related to this EST, please contact the TIGR Database  
 (tdbinfo@tdb.tigr.org)  
 Seq primer: M13 Reverse.

#### FEATURES

source

1. .251  
 Location/Qualifiers  
 /organism="Homo sapiens"  
 /db\_xref="ATCC (ihost):105130"  
 /db\_xref="taxon:9606"  
 /clone\_lib="Human prostate gland"  
 /note="Organ: prostate gland"  
 80 a 37 c 36 g 97 t 1 others

BASE COUNT

Query Match 100.0%; Score 27; DB 14; Length 251;  
 Best Local Similarity 100.0%; Pred. No. 0.12;  
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGATGATGATCACTCATGTTCTG 27  
 |||||  
 Db 119 ATGATGATGATCACTCATGTTCTG 145

RESULT 2

AW000926/c

LOCUS

DEFINITION

AW000926

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: M. Bento Soares, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Insert Length: 523 Std Error: 0.00

Seq primer: -40UP from gibco.

Location/Qualifiers

1. .426

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="IMAGE:2494968"

/clone\_lib="NCI-CGAP\_Kid11"

/lab\_host="DH10B"

/note="Organ: Kidney; Vector: pT7T3D-Pac (Pharmacia) with

a modified polylinker; Site\_1: Not I; Site\_2: Eco RI;

Plasmid DNA from the normalized library NCI-CGAP\_Kid3 was  
 prepared, and ss circles were made in vitro. Following HAP  
 purification, this DNA was used as tracer in a subtractive  
 hybridization reaction. The driver was PCR-amplified cDNAs  
 from a pool of 5,000 clones made from the same library  
 (clones 132376-132391, 145600-145675, and  
 150552-150285). Subtraction by Bento Soares and M.  
 Fatima Bonaldo.

BASE COUNT 126 a 98 c 64 g 138 t

Query Match 100.0%; Score 27; DB 10; Length 426;

Best Local Similarity 100.0%; Pred. No. 0.16;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGATGATGATCACTCATGTTCTG 27

|||||

Db 392 ATGATGATGATCACTCATGTTCTG 366

RESULT 3

N48056/c

LOCUS

DEFINITION

N48056

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (1995)

Contact: Willson RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: estevenson.wustl.edu

This clone is available royalty-free through LLNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Seq primer: m13 -40 forward

High quality sequence stop: 284.

Location/Qualifiers

1. .442

/organism="Homo sapiens"

/db\_xref="GDB:3900062"

/db\_xref="taxon:9606"

/clone="IMAGE:281686"

/clone\_lib="Soares\_multiple\_sclerosis\_2NBHMS"

/sex="male"

/tissue\_type="multiple sclerosis lesions"

/dev\_stage="Age 46"

/lab\_host="DH10B (ampicillin resistant)"

/note="Vector: pT7T3D (Pharmacia) with a modified

polylinker V-type; phagemid; Site\_1: Not I; Site\_2: Eco RI

; 1st strand cDNA was primed with a Not I - oligo(dT)

primer [5'

TGTTACCAATCTGAAGTGGAGCGCCGCAATTTTTTTTTTTT 3'],

double-stranded cDNA was size selected, ligated to Eco RI

adapters (Pharmacia), digested with Not I and cloned into

the Not I and Eco RI sites of a modified pT7T3 vector

(Pharmacia). Library went through one round of

normalization to a Cot = 5. Library constructed by Bento

Soares and M. Fatima Bonaldo. RNA from 4 multiple sclerosis

lesions from one patient was kindly provided by Dr. Kevin